

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2004, 10:36:01 ; Search time 53 Seconds
(without alignments)
3.753 Million cell updates/sec

Title: US-10-633-913-3

Perfect score: 5444

Sequence: 1 gccccagggcctgcgagaggt.....aggatcagaagttacttaccac 5444

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 811 seqs, 18271 residues

Total number of hits satisfying chosen parameters: 1622

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 817 summaries

Database : ref3.seq.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.4	0.5	35	1	ACCESSION:BB894837
2	25.4	0.5	36	1	BE894837
3	25.4	0.5	34	1	ACCESSION:BI761940
4	25.4	0.5	35	1	ACCESSION:CF315464
5	24.6	0.5	32	1	ACCESSION:CO785671
6	24.4	0.4	34	1	ACCESSION:CC887678
7	24.4	0.4	32	1	ACCESSION:AM334249
8	24.4	0.4	33	1	ACCESSION:AJ791147
9	24.4	0.4	33	1	ACCESSION:CF334899
10	23.4	0.4	33	1	ACCESSION:AZ586641
11	23.4	0.4	33	1	ACCESSION:CF291613
12	23.4	0.4	33	1	ACCESSION:CF311229
13	23.4	0.4	33	1	ACCESSION:CF326967
14	23.4	0.4	33	1	ACCESSION:CF328313
15	23.4	0.4	33	1	ACCESSION:CF336752
16	23.4	0.4	33	1	ACCESSION:CF337105
17	23.4	0.4	33	1	ACCESSION:AZ486795
18	22.6	0.4	31	1	ACCESSION:AZ627839
19	22.6	0.4	31	1	ACCESSION:AM334249
20	22.4	0.4	32	1	ACCESSION:CF291773
21	22.4	0.4	32	1	ACCESSION:CF293936
22	22.4	0.4	32	1	ACCESSION:CF309233
23	22.4	0.4	32	1	ACCESSION:CF309345
24	22.4	0.4	32	1	ACCESSION:CF313717
25	22.4	0.4	32	1	ACCESSION:CF321046
26	22.4	0.4	32	1	ACCESSION:CF328471
27	22.4	0.4	32	1	ACCESSION:CF331270
28	22.4	0.4	32	1	ACCESSION:CF332296
29	22.4	0.4	32	1	ACCESSION:AZ314322
30	22.4	0.4	32	1	ACCESSION:AZ459536
31	22.4	0.4	32	1	ACCESSION:AZ470832
32	22.4	0.4	32	1	ACCESSION:AZ611890
33	22.4	0.4	32	1	ACCESSION:AZ778018

34	22.4	0.4	32	1	DR85L21T	ACCESSION:AL986044
35	22.2	0.4	28	1	T56352	ACCESSION:T56352
36	22	0.4	30	1	AZ458127	ACCESSION:AZ458127
37	22	0.4	31	1	BO591372	ACCESSION:BO591372
38	21.6	0.4	31	1	AZ597046	ACCESSION:AZ597046
39	21.6	0.4	28	1	H68053	ACCESSION:H68053
40	21.6	0.4	29	1	AZ825156	ACCESSION:AZ825156
41	21.6	0.4	30	1	AU267300	ACCESSION:AU267300
42	21.6	0.4	30	1	AZ443322	ACCESSION:AZ443322
43	21	0.4	29	1	CF279536	ACCESSION:CF279536
44	21	0.4	29	1	CF299920	ACCESSION:CF299920
45	21	0.4	29	1	CF312601	ACCESSION:CF312601
46	21	0.4	29	1	CN545237	ACCESSION:CN545237
47	21	0.4	29	1	CN546188	ACCESSION:CN546188
48	21	0.4	29	1	CN546382	ACCESSION:CN546382
49	21	0.4	29	1	CN546438	ACCESSION:CN546438
50	21	0.4	29	1	CN546537	ACCESSION:CN546537
51	21	0.4	29	1	AZ389566	ACCESSION:AZ389566
52	21	0.4	29	1	AZ414283	ACCESSION:AZ414283
53	21	0.4	29	1	AZ451930	ACCESSION:AZ451930
54	21	0.4	29	1	AZ468402	ACCESSION:AZ468402
55	21	0.4	29	1	AZ486793	ACCESSION:AZ486793
56	21	0.4	29	1	AZ661709	ACCESSION:AZ661709
57	21	0.4	29	1	AZ784208	ACCESSION:AZ784208
58	21	0.4	29	1	AZ806470	ACCESSION:AZ806470
59	21	0.4	29	1	AZ812242	ACCESSION:AZ812242
60	21	0.4	29	1	AZ868731	ACCESSION:AZ868731
61	21	0.4	29	1	TA334090	ACCESSION:AL491938
62	21	0.4	29	1	AG193759	ACCESSION:AG193759
63	21	0.4	30	1	AL038650	ACCESSION:AL038650
64	21	0.4	30	1	BG666435	ACCESSION:BG666435
65	21	0.4	30	1	BG665511	ACCESSION:BG665511
66	21	0.4	30	1	CF280659	ACCESSION:CF280659
67	21	0.4	30	1	CF292086	ACCESSION:CF292086
68	21	0.4	30	1	CF299555	ACCESSION:CF299555
69	21	0.4	30	1	CF312417	ACCESSION:CF312417
70	21	0.4	30	1	CF322226	ACCESSION:CF322226
71	21	0.4	30	1	CF327835	ACCESSION:CF327835
72	21	0.4	30	1	CF336555	ACCESSION:CF336555
73	21	0.4	30	1	CN545845	ACCESSION:CN545845
74	21	0.4	30	1	CN545913	ACCESSION:CN545913
75	21	0.4	30	1	CN546459	ACCESSION:CN546459
76	21	0.4	30	1	CN546474	ACCESSION:CN546474
77	21	0.4	30	1	CN546789	ACCESSION:CN546789
78	21	0.4	30	1	AZ357603	ACCESSION:AZ357603
79	21	0.4	30	1	AZ455741	ACCESSION:AZ455741
80	21	0.4	30	1	AZ481739	ACCESSION:AZ481739
81	21	0.4	30	1	AZ582114	ACCESSION:AZ582114
82	21	0.4	30	1	AG191161	ACCESSION:AG191161
83	20.8	0.4	29	1	AU267990	ACCESSION:AU267990
84	20.6	0.4	27	1	AZ941721	ACCESSION:AZ941721
85	20.6	0.4	27	1	AZ970621	ACCESSION:AZ970621
86	20.6	0.4	28	1	CF307749	ACCESSION:CF307749
87	20.6	0.4	28	1	AZ824574	ACCESSION:AZ824574
88	20.6	0.4	28	1	AZ836072	ACCESSION:AZ836072
89	20.6	0.4	29	1	BO583967	ACCESSION:BO583967
90	20.2	0.4	25	1	CF317007	ACCESSION:CF317007
91	20.2	0.4	26	1	AL038686	ACCESSION:AL038686
92	20.2	0.4	26	1	CF299646	ACCESSION:CF299646
93	20.2	0.4	28	1	CF337400	ACCESSION:CF337400
94	20	0.4	28	1	A1971979	ACCESSION:A1971979
95	20	0.4	28	1	AJ666435	ACCESSION:AJ666435
96	20	0.4	28	1	AM332443	ACCESSION:AM332443
97	20	0.4	28	1	CF282351	ACCESSION:CF282351
98	20	0.4	28	1	CF321885	ACCESSION:CF321885
99	20	0.4	28	1	CF330748	ACCESSION:CF330748
100	20	0.4	28	1	CF330938	ACCESSION:CF330938
101	20	0.4	28	1	CN546364	ACCESSION:CN546364
102	20	0.4	28	1	CN546703	ACCESSION:CN546703
103	20	0.4	28	1	AZ399637	ACCESSION:AZ399637
104	20	0.4	28	1	AZ401766	ACCESSION:AZ401766
105	20	0.4	28	1	AZ471744	ACCESSION:AZ471744
106	20	0.4	28	1	AZ493138	ACCESSION:AZ493138

C 107	20	0.4	28 1	AZ653365	ACCESSION:AZ653365	180	18.2	0.3	23 1	CP334657	ACCESSION:CP334657
C 108	20	0.4	28 1	AZ785035	ACCESSION:AZ785035	C 181	18.2	0.3	23 1	CN545940	ACCESSION:CN545940
C 109	20	0.4	28 1	AZ824519	ACCESSION:AZ824519	C 182	18.2	0.3	23 1	CN546520	ACCESSION:CN546520
C 110	20	0.4	28 1	AZ833425	ACCESSION:AZ833425	C 183	18.2	0.3	23 1	COS77495	ACCESSION:COS77495
C 111	20	0.4	28 1	AZ866569	ACCESSION:AZ866569	C 184	18.2	0.3	23 1	AZ309219	ACCESSION:AZ309219
C 112	20	0.4	28 1	TA291A01Q	ACCESSION:AL486613	C 185	18.2	0.3	23 1	AZ309851	ACCESSION:AZ309851
C 113	20	0.4	28 1	TA29A09P	ACCESSION:AL453073	C 186	18.2	0.3	23 1	AZ312314	ACCESSION:AZ312314
C 114	20	0.4	28 1	TA379D11P	ACCESSION:AL497637	C 187	18.2	0.3	23 1	AZ313922	ACCESSION:AZ313922
C 115	19.8	0.4	25 1	BG929133	ACCESSION:BG929133	C 188	18.2	0.3	23 1	AZ351354	ACCESSION:AZ351354
C 116	19.8	0.4	27 1	CD028815	ACCESSION:CD028815	C 189	18.2	0.3	23 1	AZ357645	ACCESSION:AZ357645
C 117	19.8	0.4	27 1	CL654516	ACCESSION:CL654516	C 190	18.2	0.3	23 1	AZ419236	ACCESSION:AZ419236
C 118	19.6	0.4	27 1	AZ776487	ACCESSION:AZ776487	C 191	18.2	0.3	23 1	AZ461220	ACCESSION:AZ461220
C 119	19.6	0.4	27 1	AZ862643	ACCESSION:AZ862643	C 192	18.2	0.3	23 1	AZ465327	ACCESSION:AZ465327
C 120	19.6	0.4	27 1	AZ873739	ACCESSION:AZ873739	C 193	18.2	0.3	23 1	AZ481702	ACCESSION:AZ481702
C 121	19.6	0.4	27 1	TA257B07P	ACCESSION:AL483278	C 194	18.2	0.3	23 1	AZ588254	ACCESSION:AZ588254
C 122	19.4	0.4	23 1	AZ430288	ACCESSION:AZ430288	C 195	18.2	0.3	23 1	AZ593540	ACCESSION:AZ593540
C 123	19.2	0.4	25 1	AL587648	ACCESSION:AL587648	C 196	18.2	0.3	23 1	AZ610785	ACCESSION:AZ610785
C 124	19.2	0.4	25 1	AZ381039	ACCESSION:AZ381039	C 197	18.2	0.3	23 1	AZ647637	ACCESSION:AZ647637
C 125	19.2	0.4	25 1	AZ386891	ACCESSION:AZ386891	C 198	18.2	0.3	23 1	AZ654903	ACCESSION:AZ654903
C 126	19.2	0.4	26 1	AL587774	ACCESSION:AL587774	C 199	18.2	0.3	23 1	AZ787851	ACCESSION:AZ787851
C 127	19.2	0.4	26 1	R26779	ACCESSION:R26779	C 200	18.2	0.3	23 1	AZ792751	ACCESSION:AZ792751
C 128	19	0.3	27 1	AM327923	ACCESSION:AM327923	C 201	18.2	0.3	23 1	AZ859570	ACCESSION:AZ859570
C 129	19	0.3	27 1	CP291968	ACCESSION:CP291968	C 202	18.2	0.3	23 1	AZ939608	ACCESSION:AZ939608
C 130	19	0.3	27 1	CP288811	ACCESSION:CP288811	C 203	18.2	0.3	23 1	BH000534	ACCESSION:BH000534
C 131	19	0.3	27 1	CP329725	ACCESSION:CP329725	C 204	18.2	0.3	23 1	TA151C02Q	ACCESSION:AL4773028
C 132	19	0.3	27 1	CP330557	ACCESSION:CP330557	C 205	18.2	0.3	23 1	TA274B03P	ACCESSION:AL484584
C 133	19	0.3	27 1	CP335229	ACCESSION:CP335229	C 206	18.2	0.3	23 1	TA353A10P	ACCESSION:AL494456
C 134	19	0.3	27 1	CN545326	ACCESSION:CN545326	C 207	18.2	0.3	23 1	AM247159	ACCESSION:AM247159
C 135	19	0.3	27 1	CN545492	ACCESSION:CN545492	C 208	18.2	0.3	24 1	BG670391	ACCESSION:BG670391
C 136	19	0.3	27 1	CN545530	ACCESSION:CN545530	C 209	18.2	0.3	24 1	BX554611	ACCESSION:BX554611
C 137	19	0.3	27 1	CN545597	ACCESSION:CN545597	C 210	18.2	0.3	24 1	CP276855	ACCESSION:CP276855
C 138	19	0.3	27 1	CN545938	ACCESSION:CN545938	C 211	18.2	0.3	24 1	CP281313	ACCESSION:CP281313
C 139	19	0.3	27 1	CN545962	ACCESSION:CN545962	C 212	18.2	0.3	24 1	CP301561	ACCESSION:CP301561
C 140	19	0.3	27 1	CN546052	ACCESSION:CN546052	C 213	18.2	0.3	24 1	CP320862	ACCESSION:CP320862
C 141	19	0.3	27 1	CN546271	ACCESSION:CN546271	C 214	18.2	0.3	24 1	CN545249	ACCESSION:CN545249
C 142	19	0.3	27 1	CN546337	ACCESSION:CN546337	C 215	18.2	0.3	24 1	CN545307	ACCESSION:CN545307
C 143	19	0.3	27 1	CN546539	ACCESSION:CN546539	C 216	18.2	0.3	24 1	CN545657	ACCESSION:CN545657
C 144	19	0.3	27 1	CN546574	ACCESSION:CN546574	C 217	18.2	0.3	24 1	CN545784	ACCESSION:CN545784
C 145	19	0.3	27 1	N89936	ACCESSION:N89936	C 218	18.2	0.3	24 1	CN546689	ACCESSION:CN546689
C 146	19	0.3	27 1	AZ344642	ACCESSION:AZ344642	C 219	18.2	0.3	24 1	AZ328848	ACCESSION:AZ328848
C 147	19	0.3	27 1	AZ401672	ACCESSION:AZ401672	C 220	18.2	0.3	24 1	AZ363562	ACCESSION:AZ363562
C 148	19	0.3	27 1	AZ434285	ACCESSION:AZ434285	C 221	18.2	0.3	24 1	AZ386491	ACCESSION:AZ386491
C 149	19	0.3	27 1	AZ458228	ACCESSION:AZ458228	C 222	18.2	0.3	24 1	AZ390642	ACCESSION:AZ390642
C 150	19	0.3	27 1	AZ486791	ACCESSION:AZ486791	C 223	18.2	0.3	24 1	AZ438069	ACCESSION:AZ438069
C 151	19	0.3	27 1	AZ495352	ACCESSION:AZ495352	C 224	18.2	0.3	24 1	AZ458112	ACCESSION:AZ458112
C 152	19	0.3	27 1	AZ511894	ACCESSION:AZ511894	C 225	18.2	0.3	24 1	AZ459280	ACCESSION:AZ459280
C 153	19	0.3	27 1	AZ580921	ACCESSION:AZ580921	C 226	18.2	0.3	24 1	AZ621257	ACCESSION:AZ621257
C 154	19	0.3	27 1	AZ616094	ACCESSION:AZ616094	C 227	18.2	0.3	24 1	AZ644621	ACCESSION:AZ644621
C 155	19	0.3	27 1	AZ623186	ACCESSION:AZ623186	C 228	18.2	0.3	24 1	AZ786257	ACCESSION:AZ786257
C 156	19	0.3	27 1	AZ627847	ACCESSION:AZ627847	C 229	18.2	0.3	24 1	AZ834990	ACCESSION:AZ834990
C 157	19	0.3	27 1	AZ809295	ACCESSION:AZ809295	C 230	18.2	0.3	24 1	AZ970038	ACCESSION:AZ970038
C 158	19	0.3	27 1	TA355B06P	ACCESSION:AL493923	C 231	18.2	0.3	24 1	AZ984490	ACCESSION:AZ984490
C 159	18.8	0.3	23 1	AZ382013	ACCESSION:AZ382013	C 232	18.2	0.3	24 1	AZ993423	ACCESSION:AZ993423
C 160	18.8	0.3	24 1	CD743368	ACCESSION:CD743368	C 233	18.2	0.3	24 1	TA169D12P	ACCESSION:AL478922
C 161	18.8	0.3	25 1	AZ404078	ACCESSION:AZ404078	C 234	18.2	0.3	24 1	TA169D12P	ACCESSION:AL453584
C 162	18.8	0.3	25 1	AZ316353	ACCESSION:AZ316353	C 235	18.2	0.3	24 1	TA354C06P	ACCESSION:AL494439
C 163	18.8	0.3	25 1	AZ813253	ACCESSION:AZ813253	C 236	18.2	0.3	24 1	TA354C06P	ACCESSION:AL495622
C 164	18.6	0.3	25 1	CP638767	ACCESSION:CP638767	C 237	18.2	0.3	24 1	TA371E11P	ACCESSION:AL495622
C 165	18.6	0.3	25 1	N59260	ACCESSION:N59260	C 238	18.2	0.3	24 1	TA95808P	ACCESSION:AL459003
C 166	18.6	0.3	26 1	AZ355083	ACCESSION:AZ355083	C 239	18.2	0.3	25 1	AU265663	ACCESSION:AU265663
C 167	18.6	0.3	26 1	AZ437459	ACCESSION:AZ437459	C 240	18.2	0.3	25 1	CP291048	ACCESSION:CP291048
C 168	18.6	0.3	26 1	AZ623156	ACCESSION:AZ623156	C 241	18.2	0.3	25 1	CP291646	ACCESSION:CP291646
C 169	18.6	0.3	26 1	AG201580	ACCESSION:AG201580	C 242	18.2	0.3	25 1	CP299288	ACCESSION:CP299288
C 170	18.4	0.3	22 1	AZ464354	ACCESSION:AZ464354	C 243	18.2	0.3	25 1	CP300333	ACCESSION:CP300333
C 171	18.2	0.3	23 1	AJ685799	ACCESSION:AJ685799	C 244	18.2	0.3	25 1	CP301112	ACCESSION:CP301112
C 172	18.2	0.3	23 1	AJ747297	ACCESSION:AJ747297	C 245	18.2	0.3	25 1	CP316323	ACCESSION:CP316323
C 173	18.2	0.3	23 1	CP279238	ACCESSION:CP279238	C 246	18.2	0.3	25 1	CP317714	ACCESSION:CP317714
C 174	18.2	0.3	23 1	CP297943	ACCESSION:CP297943	C 247	18.2	0.3	25 1	CP319073	ACCESSION:CP319073
C 175	18.2	0.3	23 1	CP310501	ACCESSION:CP310501	C 248	18.2	0.3	25 1	CP330786	ACCESSION:CP330786
C 176	18.2	0.3	23 1	CP319212	ACCESSION:CP319212	C 249	18.2	0.3	25 1	CN545505	ACCESSION:CN545505
C 177	18.2	0.3	23 1	CP322953	ACCESSION:CP322953	C 250	18.2	0.3	25 1	CN546041	ACCESSION:CN546041
C 178	18.2	0.3	23 1	CP329042	ACCESSION:CP329042	C 251	18.2	0.3	25 1	CN546397	ACCESSION:CN546397
C 179	18.2	0.3	23 1	CP329694	ACCESSION:CP329694	C 252	18.2	0.3	25 1	CN546477	ACCESSION:CN546477

C 253	18.2	0.3	25	1	CN546728	ACCESSION:CN546728	326	17.2	0.3	22	1	AJ747407	ACCESSION:AJ747407
C 254	18.2	0.3	25	1	N33150	ACCESSION:N33150	327	17.2	0.3	22	1	AL038477	ACCESSION:AL038477
C 255	18.2	0.3	25	1	AZ344725	ACCESSION:AZ344725	328	17.2	0.3	22	1	AM332181	ACCESSION:AM332181
C 256	18.2	0.3	25	1	AZ350777	ACCESSION:AZ350777	329	17.2	0.3	22	1	AM332399	ACCESSION:AM332399
C 257	18.2	0.3	25	1	AZ389458	ACCESSION:AZ389458	330	17.2	0.3	22	1	CF299342	ACCESSION:CF299342
C 258	18.2	0.3	25	1	AZ609234	ACCESSION:AZ609234	331	17.2	0.3	22	1	CF300133	ACCESSION:CF300133
C 259	18.2	0.3	25	1	AZ623157	ACCESSION:AZ623157	332	17.2	0.3	22	1	CF310366	ACCESSION:CF310366
C 260	18.2	0.3	25	1	AZ788646	ACCESSION:AZ788646	333	17.2	0.3	22	1	CF311269	ACCESSION:CF311269
C 261	18.2	0.3	25	1	AZ832800	ACCESSION:AZ832800	334	17.2	0.3	22	1	CF311713	ACCESSION:CF311713
C 262	18.2	0.3	25	1	AZ949287	ACCESSION:AZ949287	335	17.2	0.3	22	1	CF312498	ACCESSION:CF312498
C 263	18.2	0.3	25	1	AZ980407	ACCESSION:AZ980407	336	17.2	0.3	22	1	CF330679	ACCESSION:CF330679
C 264	18.2	0.3	25	1	TA154D03P	ACCESSION:TA154D03P	337	17.2	0.3	22	1	CF333430	ACCESSION:CF333430
C 265	18.2	0.3	25	1	TA324E10P	ACCESSION:TA324E10P	338	17.2	0.3	22	1	CF334781	ACCESSION:CF334781
C 266	18.2	0.3	26	1	AJ659204	ACCESSION:AJ659204	339	17.2	0.3	22	1	CF336250	ACCESSION:CF336250
C 267	18.2	0.3	26	1	AM327613	ACCESSION:AM327613	340	17.2	0.3	22	1	CF337580	ACCESSION:CF337580
C 268	18.2	0.3	26	1	BM658913	ACCESSION:BM658913	341	17.2	0.3	22	1	CF338524	ACCESSION:CF338524
C 269	18.2	0.3	26	1	BX563414	ACCESSION:BX563414	342	17.2	0.3	22	1	CN545550	ACCESSION:CN545550
C 270	18.2	0.3	26	1	CF278359	ACCESSION:CF278359	343	17.2	0.3	22	1	AZ310066	ACCESSION:AZ310066
C 271	18.2	0.3	26	1	CF282426	ACCESSION:CF282426	344	17.2	0.3	22	1	AZ351527	ACCESSION:AZ351527
C 272	18.2	0.3	26	1	CF296851	ACCESSION:CF296851	345	17.2	0.3	22	1	AZ357630	ACCESSION:AZ357630
C 273	18.2	0.3	26	1	CF297087	ACCESSION:CF297087	346	17.2	0.3	22	1	AZ388103	ACCESSION:AZ388103
C 274	18.2	0.3	26	1	CF299701	ACCESSION:CF299701	347	17.2	0.3	22	1	AZ401908	ACCESSION:AZ401908
C 275	18.2	0.3	26	1	CF302874	ACCESSION:CF302874	348	17.2	0.3	22	1	AZ424307	ACCESSION:AZ424307
C 276	18.2	0.3	26	1	CF311369	ACCESSION:CF311369	349	17.2	0.3	22	1	AZ428818	ACCESSION:AZ428818
C 277	18.2	0.3	26	1	CF311439	ACCESSION:CF311439	350	17.2	0.3	22	1	AZ442146	ACCESSION:AZ442146
C 278	18.2	0.3	26	1	CF317311	ACCESSION:CF317311	351	17.2	0.3	22	1	AZ459654	ACCESSION:AZ459654
C 279	18.2	0.3	26	1	CN545213	ACCESSION:CN545213	352	17.2	0.3	22	1	AZ463503	ACCESSION:AZ463503
C 280	18.2	0.3	26	1	CN545225	ACCESSION:CN545225	353	17.2	0.3	22	1	AZ463652	ACCESSION:AZ463652
C 281	18.2	0.3	26	1	CN545546	ACCESSION:CN545546	354	17.2	0.3	22	1	AZ582403	ACCESSION:AZ582403
C 282	18.2	0.3	26	1	CN545723	ACCESSION:CN545723	355	17.2	0.3	22	1	AZ607658	ACCESSION:AZ607658
C 283	18.2	0.3	26	1	CN545888	ACCESSION:CN545888	356	17.2	0.3	22	1	AZ654691	ACCESSION:AZ654691
C 284	18.2	0.3	26	1	CN546608	ACCESSION:CN546608	357	17.2	0.3	22	1	AZ760533	ACCESSION:AZ760533
C 285	18.2	0.3	26	1	CN546649	ACCESSION:CN546649	358	17.2	0.3	22	1	AZ779844	ACCESSION:AZ779844
C 286	18.2	0.3	26	1	AZ342914	ACCESSION:AZ342914	359	17.2	0.3	22	1	AZ785019	ACCESSION:AZ785019
C 287	18.2	0.3	26	1	AZ359871	ACCESSION:AZ359871	360	17.2	0.3	22	1	AZ787098	ACCESSION:AZ787098
C 288	18.2	0.3	26	1	AZ376664	ACCESSION:AZ376664	361	17.2	0.3	22	1	AZ787606	ACCESSION:AZ787606
C 289	18.2	0.3	26	1	AZ389765	ACCESSION:AZ389765	362	17.2	0.3	22	1	AZ792704	ACCESSION:AZ792704
C 290	18.2	0.3	26	1	AZ414673	ACCESSION:AZ414673	363	17.2	0.3	22	1	AZ810674	ACCESSION:AZ810674
C 291	18.2	0.3	26	1	AZ593300	ACCESSION:AZ593300	364	17.2	0.3	22	1	AZ820439	ACCESSION:AZ820439
C 292	18.2	0.3	26	1	AZ612722	ACCESSION:AZ612722	365	17.2	0.3	22	1	AZ841661	ACCESSION:AZ841661
C 293	18.2	0.3	26	1	AZ624441	ACCESSION:AZ624441	366	17.2	0.3	22	1	AZ843514	ACCESSION:AZ843514
C 294	18.2	0.3	26	1	AZ627846	ACCESSION:AZ627846	367	17.2	0.3	22	1	AZ846102	ACCESSION:AZ846102
C 295	18.2	0.3	26	1	AZ635695	ACCESSION:AZ635695	368	17.2	0.3	22	1	TA131B09P	ACCESSION:TA131B09P
C 296	18.2	0.3	26	1	AZ652515	ACCESSION:AZ652515	369	17.2	0.3	22	1	TA329P10P	ACCESSION:TA329P10P
C 297	18.2	0.3	26	1	AZ800453	ACCESSION:AZ800453	370	17.2	0.3	22	1	TA35C120	ACCESSION:TA35C120
C 298	18.2	0.3	26	1	AZ963974	ACCESSION:AZ963974	371	17.2	0.3	22	1	TA380A07P	ACCESSION:TA380A07P
C 299	18.2	0.3	26	1	TA324D07P	ACCESSION:TA324D07P	372	17.2	0.3	22	1	AG194579	ACCESSION:AG194579
C 300	17.8	0.3	21	1	BX548564	ACCESSION:BX548564	373	17.2	0.3	23	1	AL038397	ACCESSION:AL038397
C 301	17.8	0.3	21	1	AZ394897	ACCESSION:AZ394897	374	17.2	0.3	23	1	AL038592	ACCESSION:AL038592
C 302	17.8	0.3	21	1	AZ486776	ACCESSION:AZ486776	375	17.2	0.3	23	1	AL038609	ACCESSION:AL038609
C 303	17.8	0.3	21	1	AZ589098	ACCESSION:AZ589098	376	17.2	0.3	23	1	AL038688	ACCESSION:AL038688
C 304	17.8	0.3	21	1	AZ597932	ACCESSION:AZ597932	377	17.2	0.3	23	1	CF300172	ACCESSION:CF300172
C 305	17.8	0.3	21	1	AZ627978	ACCESSION:AZ627978	378	17.2	0.3	23	1	CF332379	ACCESSION:CF332379
C 306	17.8	0.3	21	1	AZ828285	ACCESSION:AZ828285	379	17.2	0.3	23	1	AZ425710	ACCESSION:AZ425710
C 307	17.8	0.3	22	1	AZ633751	ACCESSION:AZ633751	380	17.2	0.3	23	1	AZ447220	ACCESSION:AZ447220
C 308	17.8	0.3	22	1	AZ822888	ACCESSION:AZ822888	381	17.2	0.3	23	1	AZ801003	ACCESSION:AZ801003
C 309	17.8	0.3	24	1	AZ627850	ACCESSION:AZ627850	382	17.2	0.3	23	1	AZ973926	ACCESSION:AZ973926
C 310	17.8	0.3	25	1	AU247142	ACCESSION:AU247142	383	17.2	0.3	24	1	TA55C06P	ACCESSION:TA55C06P
C 311	17.8	0.3	25	1	CD028814	ACCESSION:CD028814	384	17.2	0.3	24	1	CAB53764	ACCESSION:CAB53764
C 312	17.8	0.3	25	1	AZ510124	ACCESSION:AZ510124	385	17.2	0.3	24	1	CF312319	ACCESSION:CF312319
C 313	17.8	0.3	25	1	AZ659095	ACCESSION:AZ659095	386	17.2	0.3	24	1	AZ781101	ACCESSION:AZ781101
C 314	17.8	0.3	25	1	AZ644804	ACCESSION:AZ644804	387	17.2	0.3	24	1	AZ812579	ACCESSION:AZ812579
C 315	17.6	0.3	24	1	AZ399663	ACCESSION:AZ399663	388	16.8	0.3	23	1	CF296213	ACCESSION:CF296213
C 316	17.6	0.3	24	1	AZ514388	ACCESSION:AZ514388	389	16.8	0.3	23	1	AL876702	ACCESSION:AL876702
C 317	17.6	0.3	24	1	AZ670198	ACCESSION:AZ670198	390	16.6	0.3	23	1	CF297907	ACCESSION:CF297907
C 318	17.6	0.3	24	1	AZ626101	ACCESSION:AZ626101	391	16.6	0.3	23	1	CF334077	ACCESSION:CF334077
C 319	17.6	0.3	24	1	AZ814559	ACCESSION:AZ814559	392	16.6	0.3	23	1	AZ486853	ACCESSION:AZ486853
C 320	17.6	0.3	25	1	AZ330737	ACCESSION:AZ330737	393	16.6	0.3	23	1	AZ627841	ACCESSION:AZ627841
C 321	17.4	0.3	19	1	AZ510952	ACCESSION:AZ510952	394	16.6	0.3	23	1	AZ452554	ACCESSION:AZ452554
C 322	17.4	0.3	20	1	AZ433566	ACCESSION:AZ433566	395	16.6	0.3	23	1	AZ370753	ACCESSION:AZ370753
C 323	17.4	0.3	20	1	AZ492997	ACCESSION:AZ492997	396	16.6	0.3	23	1	CL693171	ACCESSION:CL693171
C 324	17.4	0.3	20	1	AZ770557	ACCESSION:AZ770557	397	16.4	0.3	19	1	AZ489586	ACCESSION:AZ489586
C 325	17.4	0.3	22	1	AJ649983	ACCESSION:AJ649983	398	16.4	0.3	19	1	AZ983014	ACCESSION:AZ983014

C 399	16.4	0.3	23	1	AZ333204	ACCESSION:AZ333204	472	15.8	0.3	20	1	AZ75620	ACCESSION:AZ75620
C 400	16.2	0.3	21	1	AJ658282	ACCESSION:AJ658282	473	15.8	0.3	20	1	AZ94997	ACCESSION:AZ94997
C 401	16.2	0.3	21	1	AJ666203	ACCESSION:AJ666203	C 474	15.8	0.3	21	1	AZ45540	ACCESSION:AZ45540
C 402	16.2	0.3	21	1	AL048777	ACCESSION:AL048777	C 475	15.8	0.3	22	1	TA28D01Q	ACCESSION:TA28D01Q
C 403	16.2	0.3	21	1	CF282216	ACCESSION:CF282216	C 476	15.6	0.3	22	1	AZ345485	ACCESSION:AZ345485
C 404	16.2	0.3	21	1	CF292703	ACCESSION:CF292703	C 477	15.6	0.3	22	1	AZ785081	ACCESSION:AZ785081
C 405	16.2	0.3	21	1	CF295642	ACCESSION:CF295642	C 478	15.6	0.3	22	1	BH000233	ACCESSION:BH000233
C 406	16.2	0.3	21	1	CF297615	ACCESSION:CF297615	C 479	15.4	0.3	18	1	BG68047	ACCESSION:BG68047
C 407	16.2	0.3	21	1	CF298322	ACCESSION:CF298322	C 480	15.4	0.3	19	1	BO594437	ACCESSION:BO594437
C 408	16.2	0.3	21	1	CF300809	ACCESSION:CF300809	C 481	15.4	0.3	18	1	CL436223	ACCESSION:CL436223
C 409	16.2	0.3	21	1	CF312715	ACCESSION:CF312715	C 482	15.4	0.3	21	1	AZ308846	ACCESSION:AZ308846
C 410	16.2	0.3	21	1	CF316073	ACCESSION:CF316073	C 483	15.4	0.3	22	1	AB094448	ACCESSION:AB094448
C 411	16.2	0.3	21	1	CF326952	ACCESSION:CF326952	C 484	15.2	0.3	20	1	AJ666402	ACCESSION:AJ666402
C 412	16.2	0.3	21	1	CF327391	ACCESSION:CF327391	C 485	15.2	0.3	20	1	AL038427	ACCESSION:AL038427
C 413	16.2	0.3	21	1	CF332956	ACCESSION:CF332956	C 486	15.2	0.3	20	1	AL038429	ACCESSION:AL038429
C 414	16.2	0.3	21	1	CF338057	ACCESSION:CF338057	C 487	15.2	0.3	20	1	AL038507	ACCESSION:AL038507
C 415	16.2	0.3	21	1	CF338552	ACCESSION:CF338552	C 488	15.2	0.3	20	1	AL038570	ACCESSION:AL038570
C 416	16.2	0.3	21	1	CN546469	ACCESSION:CN546469	C 489	15.2	0.3	20	1	AL038576	ACCESSION:AL038576
C 417	16.2	0.3	21	1	CN546504	ACCESSION:CN546504	C 490	15.2	0.3	20	1	AL038750	ACCESSION:AL038750
C 418	16.2	0.3	21	1	CN546595	ACCESSION:CN546595	C 491	15.2	0.3	20	1	AL038754	ACCESSION:AL038754
C 419	16.2	0.3	21	1	COT79794	ACCESSION:COT79794	C 492	15.2	0.3	20	1	AL038845	ACCESSION:AL038845
C 420	16.2	0.3	21	1	AZ317208	ACCESSION:AZ317208	C 493	15.2	0.3	20	1	AL587630	ACCESSION:AL587630
C 421	16.2	0.3	21	1	AZ348593	ACCESSION:AZ348593	C 494	15.2	0.3	20	1	AM334823	ACCESSION:AM334823
C 422	16.2	0.3	21	1	AZ350611	ACCESSION:AZ350611	C 495	15.2	0.3	20	1	CP280913	ACCESSION:CP280913
C 423	16.2	0.3	21	1	AZ386711	ACCESSION:AZ386711	C 496	15.2	0.3	20	1	CP282035	ACCESSION:CP282035
C 424	16.2	0.3	21	1	AZ386794	ACCESSION:AZ386794	C 497	15.2	0.3	20	1	CP282414	ACCESSION:CP282414
C 425	16.2	0.3	21	1	AZ389287	ACCESSION:AZ389287	C 498	15.2	0.3	20	1	CP298018	ACCESSION:CP298018
C 426	16.2	0.3	21	1	AZ389687	ACCESSION:AZ389687	C 499	15.2	0.3	20	1	CF299822	ACCESSION:CF299822
C 427	16.2	0.3	21	1	AZ406936	ACCESSION:AZ406936	C 500	15.2	0.3	20	1	CF301720	ACCESSION:CF301720
C 428	16.2	0.3	21	1	AZ412739	ACCESSION:AZ412739	C 501	15.2	0.3	20	1	CF302027	ACCESSION:CF302027
C 429	16.2	0.3	21	1	AZ412931	ACCESSION:AZ412931	C 502	15.2	0.3	20	1	CP308984	ACCESSION:CP308984
C 430	16.2	0.3	21	1	AZ415029	ACCESSION:AZ415029	C 503	15.2	0.3	20	1	CP310604	ACCESSION:CP310604
C 431	16.2	0.3	21	1	AZ465890	ACCESSION:AZ465890	C 504	15.2	0.3	20	1	CP313067	ACCESSION:CP313067
C 432	16.2	0.3	21	1	AZ611116	ACCESSION:AZ611116	C 505	15.2	0.3	20	1	CP313569	ACCESSION:CP313569
C 433	16.2	0.3	21	1	AZ611423	ACCESSION:AZ611423	C 506	15.2	0.3	20	1	CP319133	ACCESSION:CP319133
C 434	16.2	0.3	21	1	AZ615628	ACCESSION:AZ615628	C 507	15.2	0.3	20	1	CP321721	ACCESSION:CP321721
C 435	16.2	0.3	21	1	AZ627843	ACCESSION:AZ627843	C 508	15.2	0.3	20	1	CP328655	ACCESSION:CP328655
C 436	16.2	0.3	21	1	AZ627845	ACCESSION:AZ627845	C 509	15.2	0.3	20	1	CP333173	ACCESSION:CP333173
C 437	16.2	0.3	21	1	AZ657727	ACCESSION:AZ657727	C 510	15.2	0.3	20	1	CP334170	ACCESSION:CP334170
C 438	16.2	0.3	21	1	AZ766552	ACCESSION:AZ766552	C 511	15.2	0.3	20	1	CP336525	ACCESSION:CP336525
C 439	16.2	0.3	21	1	AZ769976	ACCESSION:AZ769976	C 512	15.2	0.3	20	1	CP337494	ACCESSION:CP337494
C 440	16.2	0.3	21	1	AZ792613	ACCESSION:AZ792613	C 513	15.2	0.3	20	1	CN545446	ACCESSION:CN545446
C 441	16.2	0.3	21	1	AZ793486	ACCESSION:AZ793486	C 514	15.2	0.3	20	1	CN545501	ACCESSION:CN545501
C 442	16.2	0.3	21	1	AZ799327	ACCESSION:AZ799327	C 515	15.2	0.3	20	1	TS0579	ACCESSION:TS0579
C 443	16.2	0.3	21	1	AZ810054	ACCESSION:AZ810054	C 516	15.2	0.3	20	1	AZ307671	ACCESSION:AZ307671
C 444	16.2	0.3	21	1	AZ815424	ACCESSION:AZ815424	C 517	15.2	0.3	20	1	AZ333980	ACCESSION:AZ333980
C 445	16.2	0.3	21	1	AZ819181	ACCESSION:AZ819181	C 518	15.2	0.3	20	1	AZ341237	ACCESSION:AZ341237
C 446	16.2	0.3	21	1	AZ821218	ACCESSION:AZ821218	C 519	15.2	0.3	20	1	AZ341530	ACCESSION:AZ341530
C 447	16.2	0.3	21	1	AZ843603	ACCESSION:AZ843603	C 520	15.2	0.3	20	1	AZ343031	ACCESSION:AZ343031
C 448	16.2	0.3	21	1	AZ853429	ACCESSION:AZ853429	C 521	15.2	0.3	20	1	AZ343730	ACCESSION:AZ343730
C 449	16.2	0.3	21	1	AZ960063	ACCESSION:AZ960063	C 522	15.2	0.3	20	1	AZ351273	ACCESSION:AZ351273
C 450	16.2	0.3	21	1	BH000837	ACCESSION:BH000837	C 523	15.2	0.3	20	1	AZ357623	ACCESSION:AZ357623
C 451	16.2	0.3	22	1	CF282024	ACCESSION:CF282024	C 524	15.2	0.3	20	1	AZ369734	ACCESSION:AZ369734
C 452	16.2	0.3	22	1	CF298427	ACCESSION:CF298427	C 525	15.2	0.3	20	1	AZ386573	ACCESSION:AZ386573
C 453	16.2	0.3	22	1	CF310486	ACCESSION:CF310486	C 526	15.2	0.3	20	1	AZ396481	ACCESSION:AZ396481
C 454	16.2	0.3	22	1	COT78290	ACCESSION:COT78290	C 527	15.2	0.3	20	1	AZ405596	ACCESSION:AZ405596
C 455	16.2	0.3	22	1	AZ304806	ACCESSION:AZ304806	C 528	15.2	0.3	20	1	AZ442328	ACCESSION:AZ442328
C 456	16.2	0.3	22	1	AZ374487	ACCESSION:AZ374487	C 529	15.2	0.3	20	1	AZ463331	ACCESSION:AZ463331
C 457	16.2	0.3	22	1	AZ505769	ACCESSION:AZ505769	C 530	15.2	0.3	20	1	AZ477734	ACCESSION:AZ477734
C 458	16.2	0.3	22	1	AZ823875	ACCESSION:AZ823875	C 531	15.2	0.3	20	1	AZ479464	ACCESSION:AZ479464
C 459	16.2	0.3	22	1	AZ845735	ACCESSION:AZ845735	C 532	15.2	0.3	20	1	AZ486784	ACCESSION:AZ486784
C 460	16.2	0.3	22	1	TA303G05P	ACCESSION:TA303G05P	C 533	15.2	0.3	20	1	AZ486787	ACCESSION:AZ486787
C 461	16.2	0.3	22	1	AL048776	ACCESSION:AL048776	C 534	15.2	0.3	20	1	AZ498625	ACCESSION:AZ498625
C 462	16.2	0.3	23	1	AL048776	ACCESSION:AL048776	C 535	15.2	0.3	20	1	AZ514729	ACCESSION:AZ514729
C 463	16.2	0.3	23	1	AL587621	ACCESSION:AL587621	C 536	15.2	0.3	20	1	AZ579122	ACCESSION:AZ579122
C 464	16.2	0.3	23	1	BO590647	ACCESSION:BO590647	C 537	15.2	0.3	20	1	AZ579178	ACCESSION:AZ579178
C 465	16.2	0.3	23	1	BX559898	ACCESSION:BX559898	C 538	15.2	0.3	20	1	AZ581208	ACCESSION:AZ581208
C 466	16.2	0.3	23	1	CF279593	ACCESSION:CF279593	C 539	15.2	0.3	20	1	AZ588011	ACCESSION:AZ588011
C 467	16.2	0.3	23	1	AZ621676	ACCESSION:AZ621676	C 540	15.2	0.3	20	1	AZ607328	ACCESSION:AZ607328
C 468	16.2	0.3	23	1	AZ817623	ACCESSION:AZ817623	C 541	15.2	0.3	20	1	AZ623155	ACCESSION:AZ623155
C 469	15.8	0.3	19	1	AI371092	ACCESSION:AI371092	C 542	15.2	0.3	20	1	AZ623214	ACCESSION:AZ623214
C 470	15.8	0.3	19	1	AZ654747	ACCESSION:AZ654747	C 543	15.2	0.3	20	1	AZ643992	ACCESSION:AZ643992
C 471	15.8	0.3	19	1	CL693177	ACCESSION:CL693177	C 544	15.2	0.3	20	1	AZ645829	ACCESSION:AZ645829

545	15.2	0.3	20	1	A2650271	ACCESSION:A2650271	C 618	14.2	0.3	19	1	CF298472	ACCESSION:CF298472
546	15.2	0.3	20	1	ACCESSION:A2760838	ACCESSION:A2760838	C 619	14.2	0.3	19	1	CF299598	ACCESSION:CF299598
547	15.2	0.3	20	1	AZ764504	ACCESSION:A2764504	C 620	14.2	0.3	19	1	CF300236	ACCESSION:CF300236
548	15.2	0.3	20	1	AZ755211	ACCESSION:A2755211	C 621	14.2	0.3	19	1	CF302327	ACCESSION:CF302327
549	15.2	0.3	20	1	AZ772091	ACCESSION:A2772091	C 622	14.2	0.3	19	1	CF302456	ACCESSION:CF302456
550	15.2	0.3	20	1	AZ779425	ACCESSION:A2779425	C 623	14.2	0.3	19	1	CF304589	ACCESSION:CF304589
551	15.2	0.3	20	1	AZ784041	ACCESSION:A2784041	C 624	14.2	0.3	19	1	CF309636	ACCESSION:CF309636
552	15.2	0.3	20	1	AZ793467	ACCESSION:A2793467	C 625	14.2	0.3	19	1	CF309801	ACCESSION:CF309801
553	15.2	0.3	20	1	AZ798529	ACCESSION:A2798529	C 626	14.2	0.3	19	1	CF309943	ACCESSION:CF309943
554	15.2	0.3	20	1	AZ805163	ACCESSION:A2805163	C 627	14.2	0.3	19	1	CF311496	ACCESSION:CF311496
555	15.2	0.3	20	1	AZ806521	ACCESSION:A2806521	C 628	14.2	0.3	19	1	CF311513	ACCESSION:CF311513
556	15.2	0.3	20	1	AZ806585	ACCESSION:A2806585	C 629	14.2	0.3	19	1	CF312403	ACCESSION:CF312403
557	15.2	0.3	20	1	AZ809306	ACCESSION:A2809306	C 630	14.2	0.3	19	1	CF315299	ACCESSION:CF315299
558	15.2	0.3	20	1	AZ810986	ACCESSION:A2810986	C 631	14.2	0.3	19	1	CF316480	ACCESSION:CF316480
559	15.2	0.3	20	1	AZ813908	ACCESSION:A2813908	C 632	14.2	0.3	19	1	CF318788	ACCESSION:CF318788
560	15.2	0.3	20	1	AZ817323	ACCESSION:A2817323	C 633	14.2	0.3	19	1	CF329136	ACCESSION:CF329136
561	15.2	0.3	20	1	AZ817414	ACCESSION:A2817414	C 634	14.2	0.3	19	1	CF329137	ACCESSION:CF329137
562	15.2	0.3	20	1	AZ817467	ACCESSION:A2817467	C 635	14.2	0.3	19	1	CF329986	ACCESSION:CF329986
563	15.2	0.3	20	1	AZ817608	ACCESSION:A2817608	C 636	14.2	0.3	19	1	CF332063	ACCESSION:CF332063
564	15.2	0.3	20	1	AZ818489	ACCESSION:A2818489	C 637	14.2	0.3	19	1	CF333507	ACCESSION:CF333507
565	15.2	0.3	20	1	AZ818816	ACCESSION:A2818816	C 638	14.2	0.3	19	1	CF333753	ACCESSION:CF333753
566	15.2	0.3	20	1	AZ837491	ACCESSION:A2837491	C 639	14.2	0.3	19	1	CF334014	ACCESSION:CF334014
567	15.2	0.3	20	1	AZ841342	ACCESSION:A2841342	C 640	14.2	0.3	19	1	CN545602	ACCESSION:CN545602
568	15.2	0.3	20	1	AZ841558	ACCESSION:A2841558	C 641	14.2	0.3	19	1	CN545922	ACCESSION:CN545922
569	15.2	0.3	20	1	AZ849506	ACCESSION:A2849506	C 642	14.2	0.3	19	1	CN545964	ACCESSION:CN545964
570	15.2	0.3	20	1	AZ858052	ACCESSION:A2858052	C 643	14.2	0.3	19	1	CN546303	ACCESSION:CN546303
571	15.2	0.3	20	1	AZ858419	ACCESSION:A2858419	C 644	14.2	0.3	19	1	AZ307313	ACCESSION:A2307313
572	15.2	0.3	20	1	AZ936914	ACCESSION:A2936914	C 645	14.2	0.3	19	1	AZ310079	ACCESSION:A2310079
573	15.2	0.3	20	1	AZ949180	ACCESSION:A2949180	C 646	14.2	0.3	19	1	AZ310105	ACCESSION:A2310105
574	15.2	0.3	20	1	AZ963973	ACCESSION:A2963973	C 647	14.2	0.3	19	1	AZ317743	ACCESSION:A2317743
575	15.2	0.3	20	1	CL680297	ACCESSION:CL680297	C 648	14.2	0.3	19	1	AZ340311	ACCESSION:A2340311
576	15.2	0.3	21	1	AL038582	ACCESSION:AL038582	C 649	14.2	0.3	19	1	AZ345499	ACCESSION:A2345499
577	15.2	0.3	21	1	AL038839	ACCESSION:AL038839	C 650	14.2	0.3	19	1	AZ350519	ACCESSION:A2350519
578	15.2	0.3	21	1	AL587702	ACCESSION:AL587702	C 651	14.2	0.3	19	1	AZ364226	ACCESSION:A2364226
579	15.2	0.3	21	1	BX556006	ACCESSION:BX556006	C 652	14.2	0.3	19	1	AZ365696	ACCESSION:A2365696
580	15.2	0.3	21	1	CF276638	ACCESSION:CF276638	C 653	14.2	0.3	19	1	AZ374409	ACCESSION:A2374409
581	15.2	0.3	21	1	CF276638	ACCESSION:CF276638	C 654	14.2	0.3	19	1	AZ374619	ACCESSION:A2374619
582	15.2	0.3	21	1	CF311914	ACCESSION:CF311914	C 655	14.2	0.3	19	1	AZ385952	ACCESSION:A2385952
583	15.2	0.3	21	1	CF318152	ACCESSION:CF318152	C 656	14.2	0.3	19	1	AZ391509	ACCESSION:A2391509
584	15.2	0.3	21	1	CF319122	ACCESSION:CF319122	C 657	14.2	0.3	19	1	AZ410050	ACCESSION:A2410050
585	15.2	0.3	21	1	AZ461717	ACCESSION:A2346717	C 658	14.2	0.3	19	1	AZ414413	ACCESSION:A2414413
586	15.2	0.3	21	1	AZ461824	ACCESSION:A2461824	C 659	14.2	0.3	19	1	AZ422604	ACCESSION:A2422604
587	15.2	0.3	21	1	AZ493766	ACCESSION:A2493766	C 660	14.2	0.3	19	1	AZ424716	ACCESSION:A2424716
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589	15.2	0.3	21	1	AZ493766	ACCESSION:A2381798	C 662	14.2	0.3	19	1	AZ442365	ACCESSION:A2442365
590	14.8	0.3	19	1	AM248747	ACCESSION:AM248747	C 663	14.2	0.3	19	1	AZ453930	ACCESSION:A2453930
591	14.8	0.3	19	1	CF334610	ACCESSION:CF334610	C 664	14.2	0.3	19	1	AZ460906	ACCESSION:A2460906
592	14.8	0.3	19	1	AZ345795	ACCESSION:A2345795	C 665	14.2	0.3	19	1	AZ471494	ACCESSION:A2471494
593	14.8	0.3	19	1	AZ513919	ACCESSION:A2513919	C 666	14.2	0.3	19	1	AZ476576	ACCESSION:A2476576
594	14.8	0.3	19	1	AZ650252	ACCESSION:A2650252	C 667	14.2	0.3	19	1	AZ486786	ACCESSION:A2486786
595	14.8	0.3	19	1	AZ650575	ACCESSION:A2650575	C 668	14.2	0.3	19	1	AZ490652	ACCESSION:A2490652
596	14.8	0.3	19	1	AZ766990	ACCESSION:A2766990	C 669	14.2	0.3	19	1	AZ508040	ACCESSION:A2508040
597	14.8	0.3	20	1	AM333777	ACCESSION:AM333777	C 670	14.2	0.3	19	1	AZ509929	ACCESSION:A2509929
598	14.8	0.3	20	1	CN754148	ACCESSION:CN754148	C 671	14.2	0.3	19	1	AZ579119	ACCESSION:A2579119
599	14.8	0.3	21	1	AJ662980	ACCESSION:AJ662980	C 672	14.2	0.3	19	1	AZ583970	ACCESSION:A2583970
600	14.8	0.3	21	1	AL048772	ACCESSION:AL048772	C 673	14.2	0.3	19	1	AZ585865	ACCESSION:A2585865
601	14.8	0.3	21	1	AZ602152	ACCESSION:A2602152	C 674	14.2	0.3	19	1	AZ593210	ACCESSION:A2593210
602	14.8	0.3	21	1	AZ610868	ACCESSION:A2610868	C 675	14.2	0.3	19	1	AZ616154	ACCESSION:A2616154
603	14.8	0.3	21	1	AZ627840	ACCESSION:A2627840	C 676	14.2	0.3	19	1	AZ627844	ACCESSION:A2627844
604	14.8	0.3	21	1	AZ764492	ACCESSION:A2764492	C 677	14.2	0.3	19	1	AZ631701	ACCESSION:A2631701
605	14.8	0.3	21	1	CL693164	ACCESSION:CL693164	C 678	14.2	0.3	19	1	AZ633821	ACCESSION:A2633821
606	14.8	0.3	21	1	CL693188	ACCESSION:CL693188	C 679	14.2	0.3	19	1	AZ643659	ACCESSION:A2643659
607	14.4	0.3	19	1	AZ353907	ACCESSION:A2353907	C 680	14.2	0.3	19	1	AZ644698	ACCESSION:A2644698
608	14.4	0.3	19	1	AJ954509	ACCESSION:AJ954509	C 681	14.2	0.3	19	1	AZ645841	ACCESSION:A2645841
609	14.2	0.3	19	1	AJ666205	ACCESSION:AJ666205	C 682	14.2	0.3	19	1	AZ648335	ACCESSION:A2648335
610	14.2	0.3	19	1	AJ666179	ACCESSION:AJ666179	C 683	14.2	0.3	19	1	AZ649888	ACCESSION:A2649888
611	14.2	0.3	19	1	AJ669138	ACCESSION:AJ669138	C 684	14.2	0.3	19	1	AZ764497	ACCESSION:A2764497
612	14.2	0.3	19	1	B0588729	ACCESSION:B0588729	C 685	14.2	0.3	19	1	AZ764532	ACCESSION:A2764532
613	14.2	0.3	19	1	CB174047	ACCESSION:CB174047	C 686	14.2	0.3	19	1	AZ764534	ACCESSION:A2764534
614	14.2	0.3	19	1	CF279008	ACCESSION:CF279008	C 687	14.2	0.3	19	1	AZ770387	ACCESSION:A2770387
615	14.2	0.3	19	1	CF291089	ACCESSION:CF291089	C 688	14.2	0.3	19	1	AZ775624	ACCESSION:A2775624
616	14.2	0.3	19	1	CF291090	ACCESSION:CF291090	C 689	14.2	0.3	19	1	AZ778858	ACCESSION:A2778858
617	14.2	0.3	19	1	CF298396	ACCESSION:CF298396	C 690	14.2	0.3	19	1	AZ779901	ACCESSION:A2779901

691	14.2	0.3	19	1	A2781876	ACCESSION:A2781876	6764	13.2	0.2	18	1	CF329484	ACCESSION:CF329484
692	14.2	0.3	19	1	A2786336	ACCESSION:A2786336	766	13.2	0.2	18	1	CF329485	ACCESSION:CF329485
693	14.2	0.3	19	1	A2787634	ACCESSION:A2787634	765	13.2	0.2	19	1	AC432757	ACCESSION:AC432757
694	14.2	0.3	19	1	A2788058	ACCESSION:A2788058	767	13.2	0.2	16	1	A1590540	ACCESSION:A1590540
695	14.2	0.3	19	1	A2789590	ACCESSION:A2789590	768	12.8	0.2	16	1	A1569544	ACCESSION:A1569544
696	14.2	0.3	19	1	A2792713	ACCESSION:A2792713	769	12.8	0.2	16	1	B0590166	ACCESSION:B0590166
697	14.2	0.3	19	1	A2795403	ACCESSION:A2795403	770	12.8	0.2	16	1	B0590507	ACCESSION:B0590507
698	14.2	0.3	19	1	A2801970	ACCESSION:A2801970	771	12.8	0.2	16	1	B0592600	ACCESSION:B0592600
699	14.2	0.3	19	1	A2822225	ACCESSION:A2822225	772	12.8	0.2	16	1	B0592965	ACCESSION:B0592965
700	14.2	0.3	19	1	A2841581	ACCESSION:A2841581	773	12.8	0.2	16	1	B0595369	ACCESSION:B0595369
701	14.2	0.3	19	1	A2841622	ACCESSION:A2841622	774	12.8	0.2	16	1	B0595717	ACCESSION:B0595717
702	14.2	0.3	19	1	A2861896	ACCESSION:A2861896	775	12.8	0.2	16	1	CF279325	ACCESSION:CF279325
703	14.2	0.3	19	1	A2936798	ACCESSION:A2936798	776	12.8	0.2	16	1	CF2966130	ACCESSION:CF2966130
704	14.2	0.3	19	1	A2962226	ACCESSION:A2962226	777	12.8	0.2	16	1	CF311057	ACCESSION:CF311057
705	14.2	0.3	19	1	A2985501	ACCESSION:A2985501	778	12.8	0.2	16	1	CF314013	ACCESSION:CF314013
706	14.2	0.3	19	1	BH000498	ACCESSION:BH000498	779	12.8	0.2	16	1	CF314377	ACCESSION:CF314377
707	14.2	0.3	19	1	AJ600883	ACCESSION:AJ600883	780	12.8	0.2	16	1	CF315789	ACCESSION:CF315789
708	14.2	0.3	19	1	CL680735	ACCESSION:CL680735	781	12.8	0.2	16	1	CF316056	ACCESSION:CF316056
709	14.2	0.3	19	1	CL685439	ACCESSION:CL685439	782	12.8	0.2	16	1	CF317718	ACCESSION:CF317718
710	14.2	0.3	19	1	CL693186	ACCESSION:CL693186	783	12.8	0.2	16	1	CF320356	ACCESSION:CF320356
711	14.2	0.3	19	1	CL693191	ACCESSION:CL693191	784	12.8	0.2	16	1	CF323722	ACCESSION:CF323722
712	14.2	0.3	20	1	AL038460	ACCESSION:AL038460	785	12.8	0.2	16	1	CF329320	ACCESSION:CF329320
713	14.2	0.3	20	1	AL587572	ACCESSION:AL587572	786	12.8	0.2	16	1	CF323386	ACCESSION:CF323386
714	14.2	0.3	20	1	AL587727	ACCESSION:AL587727	787	12.8	0.2	17	1	AM247165	ACCESSION:AM247165
715	14.2	0.3	20	1	AL587759	ACCESSION:AL587759	788	12.8	0.2	17	1	B0590687	ACCESSION:B0590687
716	14.2	0.3	20	1	CF282002	ACCESSION:CF282002	789	12.8	0.2	17	1	B0591177	ACCESSION:B0591177
717	14.2	0.3	20	1	CF299570	ACCESSION:CF299570	790	12.8	0.2	17	1	B0591588	ACCESSION:B0591588
718	14.2	0.3	20	1	CF316662	ACCESSION:CF316662	791	12.8	0.2	17	1	CF290854	ACCESSION:CF290854
719	14.2	0.3	20	1	CF318278	ACCESSION:CF318278	792	12.8	0.2	17	1	CF295807	ACCESSION:CF295807
720	14.2	0.3	20	1	CF319428	ACCESSION:CF319428	793	12.8	0.2	17	1	CF298589	ACCESSION:CF298589
721													

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC/DCID/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

Plate: LLM9748 row: d column: 06
High quality sequence start: 4
High quality sequence stop: 35.
Location/Qualifiers

FEATURES

source

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/db_xref="taxon:9606"
/clone="IMAGE:3919061"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

Query Match 0.5%; Score 25.4; DB 1; Length 35;
Best Local Similarity 82.9%; Pred. No. 33;
Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5390 ATTAATAATACAAAAAGAAAAATGAAATTA 5424
|||||
1 ATTAATAATACAAAAAGAAAAATGAAATTA 35

RESULT 2
LOCUS B1761940 36 bp mRNA linear EST 25-SEP-2001
DEFINITION 603048772F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5189224 5',
mRNA sequence.

ACCESSION B1761940
VERSION B1761940.1 GI:15753518
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 36)
NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11472 row: o column: 17
High quality sequence stop: 36.
Location/Qualifiers

FEATURES

source

1.36
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5189224"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:

PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 clones, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

Query Match 0.5%; Score 25.4; DB 1; Length 36;
Best Local Similarity 82.9%; Pred. No. 34;
Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAATTAAGG 5427
|||||
1 AAAAAATACAAAAAGAAAAATGAAATTAAGG 35

RESULT 3
LOCUS CF315464/c 34 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-04-G09.b1 OSHDAC1-overexpressing transgenic rice plasmid CDNA library (HD) Oryza sativa (japonica cultivar-group) CDNA clone HD-04-G09, mRNA sequence.

ACCESSION CF315464
VERSION CF315464.1 GI:33687225
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Bukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 34)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES

source

1.34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-04-G09"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; site 1: ScaRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice histone Deacetylase overexpression line."

Query Match 0.5%; Score 25; DB 1; Length 34;
Best Local Similarity 84.8%; Pred. No. 36;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAATTA 5425
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Db 33 AAAAAATACAAAAAGAAAAATGAAATTA 1

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RESULT 4
LOCUS      CO785671/c      35 bp      mRNA      linear      EST 05-AUG-2004
DEFINITION BL284A_H08 6-Day Axiolotl Tail Blastema (6DABL) Ambystoma mexicanum
            CDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION  CO785671
VERSION     CO785671.1  GI:51001651
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
ORGANISM    Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1 (bases 1 to 35)
AUTHORS     Haberman, B., Behn, A.G., Herklotz, S., Volkmers, M., Eckelt, K.,
            Pehlke, K., Eppert, H.H., Schackert, H.K., Wiebe, G. and Tanaka, R.M.
TITLE       An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating Blastema
            CDNA libraries
JOURNAL     Genome Biol. (2004) In press
COMMENT     Tanaka lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfluehnerstrasse 108, 01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL284A row: 08 column: H
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES
            source
            1..35
            /organism="Ambystoma mexicanum"
            /mol_type="mRNA"
            /db_xref="taxon:8296"
            /tissue_type="Tail Blastema"
            /cell_type="regenerating tail blastema"
            /clone_lib="6-Day Axiolotl Tail Blastema (6DABL)"
            /note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
            Unnormalized cDNA plasmid library prepared by Invitrogen.
            Size fractionated mRNA was poly(A) primed and cloned into
            NotI-SalI site of pCMVSPORT6. Bacterial host is
            EMDH10B-TONA. Average insert size is 1.67 kb.
            TAG_L1B=6DABL"
Query Match      0.5%; Score 25; DB 1; Length 35;
Best Local Similarity 84.8%; Pred. No. 37;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY               5393 AAAAAATACAAAAAGAAAAATGAAAAATATA 5425
Db               33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

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JOURNAL
COMMENT
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10590.
Class: TDNA tagged.
FEATURES
            source
            1..32
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /ecotype="Col-0"
            /db_xref="taxon:3702"
            /clone_lib="SALK_150577.31.20.x"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can
            be found at http://signal.salk.edu/tdna_protocols.html"
Query Match      0.5%; Score 24.6; DB 1; Length 32;
Best Local Similarity 87.1%; Pred. No. 38;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY               3981 CATCAGGCTGAGCCTGAGCTGTGAGAGCT 4011
Db               2 CTTGAAGTCTGAGCTGAGGTTGTGAGAGCT 32

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RESULT 5
LOCUS      CC887678      32 bp      DNA      linear      GSS 31-JUL-2003
DEFINITION SALK_150577.31.20 x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_150577.31.20.X, genomic
            survey sequence.
ACCESSION  CC887678
VERSION     CC887678
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 32)
            Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R.,
            Gadinna, C., Jeske, A., Karnes, M., Kim, C.O., Parker, H., Prednis, L.,
            Shin, P., Zimmermann, J. and Ecker, J.R.
            A sequence-indexed library of insertion mutations in the

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RESULT 6
LOCUS      AM334249/c      34 bp      mRNA      linear      EST 31-JAN-2000
DEFINITION S32P4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION  AM334249
VERSION     AM334249.1  GI:6830606
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
            1 (bases 1 to 34)
            Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
            Edman, J.C., Kovacs, J. and Cushion, M.
            Expressed sequence tags from Pneumocystis carinii
            Unpublished (2000)
            Contact: Staben, C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES
            source
            1..34
            /organism="Pneumocystis carinii"
            /mol_type="mRNA"
            /db_xref="taxon:4754"
            /lab_host="E. coli"
            /clone_lib="AGS-1"
            /note="Vector: Lambda Zap II; Site 1: EcoRI; Site 2: XhoI;
            P. carinii organisms (3x10e9) from a single rat (99-1-6,
            sacrificed on 3/17/99) at Cincinnati VA facilities.
            Trizol extracted RNA. Oligo dT priming, standard
            conditions described by vendor, Stratagene. Further
            details see www.uky.edu/Project/Pneumocystis/"

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Query Match 0.4%; Score 24.4; DB 1; Length 34;
 Best Local Similarity 82.4%; Pred. No. 43;
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5382 ATTGAAGATTAAAAATGCAAAAAAGAAAAA 5415
 |||||
 34 ATTAAAAAAGAAAAAAGAAAAA 1

RESULT 7
 AJ791147/c 32 bp mRNA linear EST 09-AUG-2004
 LOCUS AJ791147 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
 DEFINITION 018.2.07.001, mRNA sequence.

ACCESSION AJ791147.1 GI:51061240
 VERSION EST.
 KEYWORDS Antirrhinum majus (snapdragon)
 SOURCE Antirrhinum majus

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae;
 Antirrhinum.
 1 (bases 1 to 32)

REFERENCE Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
 Antirrhinum EST collection
 TITLE Unpublished (2003)
 JOURNAL Contact: Schwarz-Sommer Z.
 COMMENT Molekulare Pflanzen-genetik
 MPI fuer Zuechtungs-forschung
 Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES
 source Location/Qualifiers

1..32
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
 /db_xref="taxon:4151"
 /clone="018.2.07.001"
 /issue_type="Whole plant"
 /clone_lib="Antirrhinum majus whole plant"

Query Match 0.4%; Score 24; DB 1; Length 32;
 Best Local Similarity 84.4%; Pred. No. 45;
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5394 AAAAATACAAAAAGAAAAATGAAATGAA 5425
 |||||
 32 AAAAAAAGAAAAAAGAAAAA 1

RESULT 8
 CF334899/c 33 bp mRNA linear EST 16-AUG-2003
 LOCUS CF334899 Oryza sativa (japonica cultivar-group) cDNA clone
 DEFINITION JMT--04-F19.g1 AtCMT-overexpressing transgenic rice plasmid cDNA
 JMT--04-F19, mRNA sequence.

ACCESSION CF334899.1 GI:33818141
 VERSION EST.
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Buritardidae; Oryzaceae; Oryza.

1 (bases 1 to 33)
 Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Klm,J.K., Klm,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

0.4%;
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source

1..33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39847"
 /clone="JMT--04-F19"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="B.col1 DH10B"
 /clone_lib="AtCMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.4%; Score 24; DB 1; Length 33;
 Best Local Similarity 84.4%; Pred. No. 47;
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5394 AAAAATACAAAAAGAAAAATGAAATGAA 5425
 |||||
 33 AAAAAAAGAAAAAAGAAAAA 2

RESULT 9
 AZ586641 33 bp DNA linear GSS 13-DEC-2000
 LOCUS AZ586641 clone UGCG1M0392N08 R, genomic survey sequence.
 DEFINITION 1M0392N08R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0392N08 R, genomic survey sequence.

ACCESSION AZ586641.1 GI:11708831
 VERSION GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 33)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Iselm,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center.
 University of Utah
 Rm. 308, Biomedical Polymer Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0392 row: N column: 08
 Seq primer: CACACAGAAACAGCATATGACC
 Class: plasmid ends
 High quality sequence strop: 33.
 Location/Qualifiers

FEATURES
 source

1..33
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0392N08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv, Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 24; DB 1; Length 33;
Best Local Similarity 84.4%; Pred. No. 47;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5384 TTAAGATTAAAAATACAAAAAGAAAAA 5415
DB 2 TTAATATATTTAAAAATTTAAAAAGAAAAA 33

RESULT 10
CF291613/c 33 bp mRNA linear EST 14-AUG-2003
LOCUS 14R00T--02-B21.b1 Rice root plasmid cDNA library (14R00T) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14R00T--02-B21, mRNA
sequence.
ACCESSION CF291613
VERSION CF291613.1 GI:33660646
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..33
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14R00T--02-B21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14R00T)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAATATA 5425
DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11
CF311229/c 33 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--06-F23.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-F23, mRNA sequence.
ACCESSION CF311229
VERSION CF311229.1 GI:33682990
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..33
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/dev_stage="14 days after germination"
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cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABF-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.4%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAATGAAATATA 5425
DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 12
CF326967/c 33 bp mRNA linear EST 18-AUG-2003
LOCUS NAC1--01-B04.b1 Rice callus plasmid cDNA library (NAC1) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NAC1--01-B04, mRNA
sequence.
ACCESSION CF326967
VERSION CF326967.1 GI:33802189
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 33)

Query Match 0.4%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of BioScience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
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 /organism="Oryza sativa (japonica cultivar-group)"
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 /clone="NACL--01-B04"
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 /lab_host="E.coli DH10B"
 /note="Vector: PCR4-TOPO, Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 23.4; DB 1; Length 33;
 Best Local Similarity 81.8%; Pred. No. 56;
 Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Query Match 0.4%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 13 CF328313 33 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--03-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--03-C14, mRNA
 sequence.
ACCESSION CF328313 GI:33804873
VERSION CF328313
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 33)
 Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of BioScience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--03-C14"
 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /note="Vector: PCR4-TOPO, Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 23.4; DB 1; Length 33;
 Best Local Similarity 81.8%; Pred. No. 56;
 Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 14 CF336752/c 33 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--06-019.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--06-019, mRNA sequence.
ACCESSION CF336752 GI:33821884
VERSION CF336752
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 33)
 Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of BioScience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.4%; Score 23.4; DB 1; Length 33;
 Best Local Similarity 81.8%; Pred. No. 56;
 Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Query Match 0.4%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 15 CF337105/c 33 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--07-G18.b1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--07-G18, mRNA sequence.
ACCESSION CF337105 GI:33822596
VERSION CF337105
KEYWORDS EST.

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Query Match	Best Local Similarity 81.8%; Pred. No. 56;	0.4%; Score 23.4; DB 1; Length 33;				
Matches 27; Conservative	0; Mismatches 6; Indels 0; Gaps 0;					
Ox	5393 AAAAAAAAAAAGAAAAATGAAATATAA 5425					
Db	33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1					
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LOCUS	1M0315P22P Mouse 10kb plasmid UUC1M library Mus musculus genomic					
DEFINITION	clone UUC1M0315P22 F, genomic survey sequence.					
ACCESSION	AZ486795					
VERSION	AZ486795.1	GI:10653918				
KEYWORDS	GSS.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
AUTHORS	1 (bases 1 to 33)					
	Dunn, P., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Isliam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.					
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0315 Row: P Column: 22					

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Seq primer: CGTTGTAAGACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G114732114[g5]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAAAGAAAAATTA 5425
Dn 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 17
AZ627839/c 33 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
1M0474B02P Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0474B02 F, genomic survey sequence.
ACCESSION
AZ627839
VERSION
AZ627839.1 GI:11750125
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Jellam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Niederhuesern,A., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhuesern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: B column: 02
Seq primer: CGTTGTAAGACGACGGCCAGT

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Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UTGCM0474B02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCM library"
/note="Vector: pMD22m; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 5393 AAAAAATACAAAAAGAAAAATGAATTA 5425
DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 18
LOCUS AU268044 31 bp mRNA linear EST 26-APR-2004
DEFINITION AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA
SEQUENCE
ACCESSION AU268044 GI:20526842
VERSION AU268044
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE 1 (bases 1 to 31)
AUTHORS Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,R., Ochiai,H., Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
TITLE Analyses of cDNAs from growth and slug stages of Dictyostelium discoideum
JOURNAL Nucleic Acids Res. 32 (5), 1647-1653 (2004)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
1..31
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH836"
/sex="mat A"

/dev_stage="vegetative"
/clone_1lb="VS"

Query Match 0.4%; Score 22.6; DB 1; Length 31;
Best Local Similarity 86.2%; Pred. No. 65;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5397 AATATCAAAAAAGAAAAATGAATTA 5425
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 19
LOCUS AW327277 32 bp mRNA linear EST 28-JAN-2000
DEFINITION AW327277.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846628 5', mRNA
SEQUENCE
ACCESSION AW327277 GI:6797772
VERSION AW327277
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 32)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Edge Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Plate: LHC00028 row: G column: 13
Seq primer: -21m13 forward primer (ABI).
Location/Qualifiers
1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2846628"
/issue_type="T cell leukemia"
/cell_line="MGC2"
/clone_1lb="NIH MGC_2"
/note="Organ: Blood; Vector: pOTB7a; Library prepared by Edge Biosystems."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
Best Local Similarity 81.2%; Pred. No. 72;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 5393 AAAAAATACAAAAAGAAAAATGAATTA 5424
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 20
LOCUS CF291773/c 32 bp mRNA linear EST 14-AUG-2003
DEFINITION CF291773 14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-F12, mRNA
SEQUENCE
ACCESSION CF291773 GI:33660806
VERSION CF291773
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 32)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ROOT--02-F12"
 /issue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 72;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAAAATGAATAA 5424
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 21
 CF299386/c 32 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-G07, mRNA
 sequence.
 ACCESSION CF299386
 VERSION CF299386
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 /clone="7LEAF--03-G07"
 /issue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 72;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 22
 CF309233 32 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--03-F14, mRNA sequence.
 ACCESSION CF309233
 VERSION CF309233
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..32
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABF-responsve
 element binding transcription factor 3 overexpression
 line."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 72;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAAAATGAATAA 5424
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 23
 CF309345 32 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF--03-I03.b1 ABF3-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--03-I03, mRNA sequence.

ACCESSION CP309345
 VERSION CP309345.1 GI:33681106
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 1..32
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 /clone="ABF--03-103"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 72;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OR 5393 AAAAAATACAAAAAGAAAAATGAATTA 5424
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 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 24
 CP313717/c 32 bp mRNA linear EST 15-AUG-2003
 LOCUS HD--01-P05.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 DEFINITION HD--01-P05, mRNA sequence.
 ACCESSION CP313717.1 GI:33685478
 VERSION CP313717
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers
 1..32
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /clone="HD--01-P05"
 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 72;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OR 5393 AAAAAATACAAAAAGAAAAATGAATTA 5424
 ||||| ||||| ||||| ||||| |||||
 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 25
 CP321046/c 32 bp mRNA linear EST 15-AUG-2003
 LOCUS HD--12-C15.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 DEFINITION HD--12-C15, mRNA sequence.
 ACCESSION CP321046.1 GI:33692807
 VERSION CP321046
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
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 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
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 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 72;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Matches	26;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
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DEFINITION	NACLT--03-G09.b1 Rice callus plasmid cDNA library (NACLT) Oryza sativa (japonica cultivar-group) CDNA clone NACLT--03-G09, mRNA sequence.								
ACCESSION	CF328471			32 bp	mRNA		linear	EST 18-AUG-2003	
VERSION	CF328471.1			GI:33805189					
SOURCE	EST.								
ORGANISM	Oryza sativa (japonica cultivar-group)								
	Oryza sativa (japonica cultivar-group)								
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.								
REFERENCE	1 (bases 1 to 32)								
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.								
TITLE	Large-scale Sequencing Analysis of Rice ESTs								
JOURNAL	Unpublished (2003)								
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.								
FEATURES	location/gb10.com, bhnahm@bio.myongji.ac.kr.								
source	Location/Qualifiers								
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	/cultivar="Nackdong"								
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	/tissue_type="callus"								
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	/lab_host="E.coli DH10B"								
	/clone_lib="Rice callus plasmid cDNA library (NACLT)"								
	/note="Vector: pCR4-TOPo; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."								
Query Match	0.4%; Score 22.4; DB 1; Length 32;								
Best Local Similarity	81.2%; Pred. No. 72;								
Matches	26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;								
OY	5393	AAAAAAAAATGCAAAAAAGAAAATACTAA	5424						
Db	32	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1						
LOCUS	CF331270/c								
DEFINITION	NACLT--07-F08.b1 Rice callus plasmid cDNA library (NACLT) Oryza sativa (japonica cultivar-group) CDNA clone NACLT--07-F08, mRNA sequence.								
ACCESSION	CF331270								
VERSION	CF331270.1								
KEYWORDS	GI:33810751								
SOURCE	EST.								
ORGANISM	Oryza sativa (japonica cultivar-group)								
	Oryza sativa (japonica cultivar-group)								
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.								
REFERENCE	1 (bases 1 to 32)								
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,								

```

TITLE
JOURNAL
COMMENT
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
/db_xref="taxon:39947"
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/dev stage="proliferated callus on 2M6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="vector: pCR4-TOPO; site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 22.4; DB 1; Length 32;
Best Local Similarity 81.2%; Pred. No. 72;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0

Oy      5393 AAAAAAAAAAGAAAAATGAAATAA 5424
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Db       32 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 28
CF332296/c
LOCUS
DEFINITION
CF332296          32 bp      mRNA      linear      EST 18-AUG-2003
NACL--08-M01.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) CDNA clone NACL--08-M01, mRNA
sequence.
CF332296
CF332296.1 GI:33812816
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Embryophyta; Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.U., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/tissue type="callus"
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/lab_host="E.coli DH10B"
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/note="vector: pCR4-TOPO; site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

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RT-PCR."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 72;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5383 TTTAAGATTAAATAAAGAAAAA 5414
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 32 TTTCAGAAAAAATTAATAAATAAATAA 1

RESULT 29
 AZ314322 32 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ314322/c
 DEFINITION 1M0031N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0031N05 F, genomic survey sequence.
 ACCESSION AZ314322
 VERSION AZ314322.1 GI:10360096
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: N column: 05
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 32.

FEATURES
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 /strain="C57BL/6J"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 72;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5394 AAAAAATCAAAAAAATGAATAATAA 5425
 |||||
 32 AAAAAAATCAAAAAAATGAATAATAA 1

RESULT 30
 AZ459536 32 bp DNA linear GSS 04-OCT-2000
 LOCUS AZ459536/c
 DEFINITION 1M0264M16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0264M16 F, genomic survey sequence.
 ACCESSION AZ459536
 VERSION AZ459536.1 GI:10617577
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0264 row: M column: 16
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 32.

FEATURES
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 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0264M16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
Best Local Similarity 81.2%; Pred. No. 72;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAATGAATTA 5424
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 31
AZ470832 32 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0285F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0285F14 F, genomic survey sequence.
ACCESSION AZ470832
VERSION AZ470832.1 GI:10628957
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 32)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0265 row: F column: 14
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers

FEATURES
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

0.4%; Score 22.4; DB 1; Length 32;

Best Local Similarity 81.2%; Pred. No. 72;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAATGAATTA 5424
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 32

RESULT 32
AZ611890 32 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0438E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0438E02 R, genomic survey sequence.
ACCESSION AZ611890
VERSION AZ611890.1 GI:11734080
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 32)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0438 row: E column: 02
Seq primer: CACACGAAACAGCTAGTACCC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers

FEATURES
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/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

0.4%; Score 22.4; DB 1; Length 32;
Best Local Similarity 81.2%; Pred. No. 72;

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAATGAAATTA 5424

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 33

LOCUS A2778018

DEFINITION 2M0012020R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM2M0012020 R, genomic survey sequence.

ACCESSION A2778018

VERSION A2778018

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 32)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0012 row: 0 column: 20
Seq primer: CACACAGGAACACGTATGAC
Clase: plasmid ends
High quality sequence stop: 32.

FEATURES

source

1..32
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM2M0012020"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCM library"
/note="Vector: FMD2M; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[14732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 22.4; DB 1; Length 32;
Best Local Similarity 81.2%; Pred. No. 72;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAATGAAATTA 5424

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 34

LOCUS DR85L21T

DEFINITION Danio rerio genomic clone DKEX-85L21, genomic survey sequence.

ACCESSION AL986044

VERSION AL986044.1

KEYWORDS GSS.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. 1 (bases 1 to 32)

AUTHORS Humphray, S.J., Huckle, B. and Hunt, S.E.

TITLE Direct Submission

JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquerry@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 85L21. 85L21 is part of the Daniokey BAC library created by R. Plaetzer and N.V. Keygene.

FEATURES

source

1..32
Location/Qualifiers

/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-85L21"
/issue_type="Testis"
/note="vector pindigobAC-536"

Query Match 0.4%; Score 22.4; DB 1; Length 32;
Best Local Similarity 81.2%; Pred. No. 72;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAATGAAATTA 5424

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 35

LOCUS T56352C

DEFINITION yb34c09.g1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73072.3, similar to gb:541458.RD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT (HUMAN), mRNA sequence.

ACCESSION T56352

VERSION T56352.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, W., Le, M., Le, N., Marls, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.P., Chappel, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, W., Le, M., Le, N., Marls, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

PUBMED 8889549

COMMENT Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -21m13
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:494737"
/db_xref="taxon:9606"
/clone="IMAGE:73072"
/tissue_type="fetal spleen"
/dev_stage="fetal"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene fetal spleen (#937205)"
/note="Organ: spleen; Vector: pBluescript SK-; Site: 1;
ECORI; Site 2: XhoI; Cloned unidirectionally.
Oligo dr. Pooled spleens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG
3' -3' adaptor sequence: 5' CTCAGTTTCTTTTCTTTT 3' "

Query Match 0.4%; Score 22.2; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5394 AAAAAATACAAAAAGAAAAATGAAA 5421
|||||
Db 28 AAAAAAAAAAAAAAAAAATNAAA 1

RESULT 36
AZ458127/c 30 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
1M0261124R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0261124 R, genomic survey sequence.
ACCESSION
AZ458127
VERSION
AZ458127.1 GI:10616252
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Place: 0261 row: 1 column: 24
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 22; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5395 AAAAAATACAAAAAGAAAAATGAAATGA 5424
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 37
B0591372/c 31 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
E012712-024-017-115-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-115 3-PRIME, mRNA sequence.
ACCESSION
B0591372
VERSION
B0591372.1 GI:26120955
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
1 (bases 1 to 31)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfach, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehnach, H.
and Radelof, U.
Construction of a 'unigenes' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED
12472698
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 31 Std Error: 0.00
Place: 17 row: 1 column: 15
Seq primer: T7; GTAATACGACCTCATATGAGGC.
Location/Qualifiers
1..31
/organism="Beta vulgaris"
/mol_type="mRNA"

FEATURES

source

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/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="GABI:188741"
/db_xref="taxon:161934"
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/lab_host="EMDHI08"
/clone_lib="WPIZ-ADIS-024-storage root"
/notes="Vector: PCWVS/PORT6; Site 1: Sali; Site 2: Noct;
cDNA library from sugar beet, library provided by KWS
Kleimanzieneener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-Noct, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-Noct-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 22; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5396 AAAATATCAAAAAGAAAAATGAAAAAT 5425
DB 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 38
A2597046 31 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0410K08 Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0410K08 R, genomic survey sequence.
ACCESSION A2597046.1 GI:11719236
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 31)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunng@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: K column: 08
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloname="UGCGIM0410K08"
/sex="Male"
/lab_host="R. Coit strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

```

```

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI:4732114|9D|AF12072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.4%; Score 22; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAATATCAAAAAGAAAAATGAAAT 5422
DB 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 39
H68053 28 bp mRNA linear EST 18-OCT-1995
LOCUS Y74F04.r1 Soares fetal liver spleen INF15 Homo sapiens cDNA clone
DEFINITION IMAGE:211039 5' similar to gb:U04970 CARBOXYPEPTIDASE M PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION H68053.1 GI:1026793
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 28)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M. P., Chapple, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hiltman, M., Kucaba, T., Lacy, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L.,
Roehlfing, T., Scheinberg, K., Soares, M. B., Tan, F., Thierry-Mieg, J.,
Trevaaskis, B., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Unpublished (1996)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 653
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL.
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 653 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:378380"

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	/db_xref="taxon:9606"	
	/clone="IMAGE:211039"	
	/sex="male"	
	/dev_stage="20 week-post conception fetus"	
	/lab_host="DH10B (ampicillin resistant)"	
	/clone_lib="Soares fetal liver spleen mPLS"	
	/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACGGAAGAATTAATTAAAGACTCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."	
Query Match	0.4%; Score 21.6;	DB 1; Length 28;
Best Local Similarity	85.7%; Pred. No. 78;	
Matches 24; Conservative	0; Mismatches	4; Indels 0; Gaps 0;
Oy	3589 CATGTGCTCAGGGCTAATCTCAATCC	3616
Db	28 CATGTGCTCAGGGCTGCTTGAACTCC	1

RESULT 40					
AZ825156					
LOCUS	AZ825156	29 bp	DNA	linear	GSS 20-FEB-2001
DEFINITION	2M0100N08F Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06G2M0100N08 F, genomic survey sequence.				

ACCESSION	AZ825156
VERSION	AZ825156.1
	GI:12995064

KEYWORDS: GSS.

SOURCE ORGANISM	Mus musculus (house mouse)
Mus musculus	

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)

Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
plasmid inserts
unpublished (2000)
Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0100 row: N column: 08
 Seq primer: CATTGTAAACACACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES	Location/Qualifiers
source	1. .29

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2M01.00N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/vector="PMD43n1; Purified genomic DNA from M.
musculus C57BL/6J male" was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnars/). The DNA
was hydrolytically sheared by repeated passage through a

```

Query Match	0.4%	Score 21.6	DB 1	Length 29
Best Local Similarity	85.7%	Pred. No. 81		
Matches	24	Conservative	0	Mismatches 4; Indels 0; Gaps 0.
QY	5394	AAAAAAAAAGAAAAATGAAA	5421	
DB	1	AAAAAAAAAAAAAAAAATAAAA	28	

RESULT	41				
AU267300					
LOCUS					
DEFINITION					
	AU267300	30 bp	mrna	linear	EST 26-APR-2004
	AU267300 VS	Dictyostellium	discoideum	cdna	clone VSH345 5', mrna
	Sequence.				

ACCESSION	AU267300	GI:20526098
VERSION	AU267300.1	
KEYWORDS	EST.	

SOURCE

ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 30)	Urushihara, H., Morio, T., Saito, T., Kohara, Y., Korki, E., Ochiai, H.	
	Maeda, M., Williams, J.G., Takeuchi, I. and Tanaka, Y.	
		Analyses of cDNAs from growth and slug stages of <i>Dicystosellum</i>

JOURNAL COMMENT
 ascoidem
 Nucleic Acids Res. 32 (5), 1647-1653 (2004)
 Contact: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba

University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES	location/Qualifiers
source	1. .30

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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/strain="XX4"
/db_xref="taxon:44689"
/c1one="VSH345"
/bex="mat A"
/dev_stage="vegetative"
/c1one_id="VS"

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Query Match	0.4%	Score 21.6;	DB 1;	Length 30;
Best Local Similarity	82.8%	Pred. No. 84;		
Matches	24;	Conservative	0;	Mismatches 5;
				Indels 0;
				Gaps 0.

QY 5397 AAATACAAAAAGAAAAATGAAATAAA 5425
||| | ||||| ||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAAAAAAAAATNAAAAAAAA 29

RESULT 42	
A2443322	
LOCUS	30 bp DNA linear
DEFINITION	GS5 04-OCT-2000
	106237L20R Mouse 10kb plasmid UUC1M library Mus musculus genomic
	clone UUC1M0237L20 R, genomic survey sequence.

ACCESSION AZ443322
 VERSION AZ443322.1 GI:10591190
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 30)
 Durr, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Place: 0237 row: 1 Column: 20
 Seq primer: CACACAGAAACAGCATATGACC
 Class: plasmid ends
 High quality sequence stop: 30.
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 1. 30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U00C1M0237L20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid U00C1M library"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21.6; DB 1; Length 30;
 Best Local Similarity 85.7%; Pred. No. 84;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAAAGAAAAATGAAA 5420
 ||||| ||||| ||||| ||||| |||||
 Db 3 AAAAAAAAAAAGAAAAATGAAA 30

RESULT 43
 CF279536 29 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--05-N22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-N22, mRNA sequence.

ACCESSION CF279536
 VERSION CF279536.1 GI:33656922
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriactoidae; Oryzaceae; Oryza.
 1 (bases 1 to 29)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 321 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 FEATURES
 source
 1. 29
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--05-N22"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E. coli DH10B"
 /clone_1lb="Rice etiolated leaf plasmid cDNA library (14ETL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 21; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 96;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421
 ||||| ||||| ||||| ||||| |||||
 Db 29 AAAAAAAAAAAGAAAAATGAAA 1

RESULT 44
 CF299920 29 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--04-C02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C02, mRNA sequence.
 ACCESSION CF299920
 VERSION CF299920.1 GI:33671681
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriactoidae; Oryzaceae; Oryza.
 1 (bases 1 to 29)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 321 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 FEATURES
 source
 1. 29


```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF-04-C02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match 0.4%; Score 21; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 96;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAATGCAGAAAAAATGAAA 5421
 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 45
 CFJ12601 29 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF--08-G22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--08-G22, mRNA sequence.

ACCESSION CFJ12601.1 GI:33684362
 VERSION CFJ12601.1
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.U., Kim,M.U., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers
 1..29
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--08-G22"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.4%; Score 21; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 96;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAATGCAGAAAAAATGAAA 5421
 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 46
 CN545237/c 29 bp mRNA linear EST 30-APR-2004
 LOCUS EST 17181 Green Grape Skin Triplex2 library vitis vinifera cDNA
 DEFINITION clone B3CS00GL004G11 3', mRNA sequence.

ACCESSION CN545237
 VERSION CN545237.1 GI:46909862
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 29)
 Abbal,P., Agasse,A., Agorgeres,A., Atanasova,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)

JOURNAL CONTACT: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: 17.
 Location/Qualifiers
 1..29
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS00GL004G11"
 /dev_stage="green stage"
 /clone_lib="green stage"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
 SfilA; Site_2: SfilB; Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 96;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAATGCAGAAAAAATGAAA 5421
 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 47
 CN546188/c 29 bp mRNA linear EST 30-APR-2004
 LOCUS EST 18140 Ripe Grape Skin Triplex2 library vitis vinifera cDNA
 DEFINITION clone B3CS00RL009D04 3', mRNA sequence.

ACCESSION CN546188
 VERSION CN546188.1 GI:46910813
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 29)
 Abbal,P., Agasse,A., Agorgeres,A., Atanasova,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)

COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="rRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS08RL009D04"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2, Site_1:
SfiIA; Site_2: SfiIB, Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421
|||||
29 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 48
CN546382/c
LOCUS 29 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18335 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
ACCESSION CN546382
CDNA clone B3CS1XGB016D07 3', mRNA sequence.
VERSION CN546382.1 GI:46911007
KEYWORDS EST
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 29)
Abbel,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Texier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="rRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB016D07"
/dev_stage="green stage"
/clone_1lb="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2, Site_1: SfiIA; Site_2: SfiIB, Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421
|||||
29 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 49
CN546438/c
LOCUS 29 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18582 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
ACCESSION CN546438
CDNA clone B3CS57RB007A03 3', mRNA sequence.
VERSION CN546438.1 GI:46911063
KEYWORDS EST
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 29)
Abbel,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Texier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="rRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007A03"
/dev_stage="ripe stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2, Site_1: SfiIA; Site_2: SfiIB, Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421
|||||
29 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 50
CN546557/c
LOCUS 29 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18701 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
ACCESSION CN546557
CDNA clone B3CS58RB008C10 3', mRNA sequence.
VERSION CN546557.1 GI:46911182
KEYWORDS EST
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.

```

REFERENCE      1 (bases 1 to 29)
AUTHORS        Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,
                Couture, C., Dedaldecamp, F., Delrot, S., Gillesant, D., Grimplet, J.,
                Hamdi, S., Komieu, C. and Terrier, N.
TITLE          Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
                or seeds) at Various Developmental Stages
JOURNAL        Unpublished (2002)
COMMENT        Contact: Hamdi S.
                UMR 619 - Equipe Biologie de la Vigne
                Universite de Bordeaux I, Institut National de la Recherche
                Agronomique
                71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                France
                Tel: 00-33-(0)5-57-12-25-50
                Fax: 00-33-(0)5-57-12-25-48
                Email: s.hamdi@bordeaux.inra.fr
                Seq primer: T7.
FEATURES
  source       Location/Qualifiers
                1..29
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultur="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clone="B3CS38RB008C10"
                /dev_stage="ripe stage"
                /clone_1ib="Ripe Grape Berry Lambda Triplex2 Library"
                /note="Organ: Fruit without seeds; Vector: Lambda
                Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"
Query Match      0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy              5393 AAAAAAAAAACAAAGAAAGAAATGAAAA 5421
Db              1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
                ||||| ||||| ||||| ||||| |||||
RESULT 51
LOCUS      A2389566                29 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION 1M0150D21P Mouse 10kb plasmid UGCGIM library Mus musculus genomic
ACCESSION  A2389566
VERSION     A2389566.1 GI:10503274
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 29)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weis, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0150 row: D column: 21
            Seq primer: CGTGTAAACGACGCGCCAGT
            Class: plasmid ends
            High quality sequence atp: 29.
FEATURES
  source       Location/Qualifiers
                1..29

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0150D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 [g1473214|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy              5393 AAAAAAAAAACAAAGAAAGAAATGAAAA 5421
Db              1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29
                ||||| ||||| ||||| ||||| |||||
RESULT 52
LOCUS      A2414283                29 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION 1M0186G12R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
ACCESSION  A2414283
VERSION     A2414283.1 GI:10538296
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 29)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weis, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0188 row: G column: 12
            Seq primer: CACACAGAAACAGCTATAGACC
            Class: plasmid ends
            High quality sequence atp: 29.
FEATURES
  source       Location/Qualifiers
                1..29
                /organism="Mus musculus"

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/mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0251B05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 96;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAATGAAA 5421
 Db 29 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 53
 AZ451930/c 29 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0251B05R Mouse 10kb plasmid UGGCM library Mus musculus genomic
 DEFINITION clone UGGCM0251B05 R, genomic survey sequence.

ACCESSION AZ451930
 VERSION AZ451930.1 GI:10608203
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 29)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddun@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0251 row: B column: 05
 Seq primer: CACACAGAAACGATATGAC
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"

/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0251B05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 96;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAATGAAA 5421
 Db 29 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 54
 AZ468402/c 29 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0281G24F Mouse 10kb plasmid UGGCM library Mus musculus genomic
 DEFINITION clone UGGCM0281G24 F, genomic survey sequence.

ACCESSION AZ468402
 VERSION AZ468402.1 GI:10626527
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 29)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddun@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0281 row: G column: 24
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES
 source 1..29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0315N21"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 96;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5421
 Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 55
 AZ486793/c 29 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0315N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0315N21 F, genomic survey sequence.
 ACCESSION AZ486793
 VERSION AZ486793.1 GI:10653915
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: N column: 21
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES
 source Location/Qualifiers
 1..29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"

/clone="UUGC1M0315N21"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 96;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5421
 Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 56
 AZ661709/c 29 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0540K20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0540K20 F, genomic survey sequence.
 ACCESSION AZ661709
 VERSION AZ661709.1 GI:11798855
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0540 row: K column: 20
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES
 source Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0540K20"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1[473214]gb[AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAAAATGAAA 5421
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 57
LOCUS AZ784208 29 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0026113R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0026113 R, genomic survey sequence.
ACCESSION AZ784208
VERSION AZ784208.1 GI:12919703
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: I column: 13
Seq primer: CACACAGAAACAGCTATGACC
Classes: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0026113"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1[473214]gb[AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAAAATGAAA 5421
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 58
LOCUS AZ806470 29 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0068102R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0068102 R, genomic survey sequence.
ACCESSION AZ806470
VERSION AZ806470.1 GI:12969849
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: I column: 02
Seq primer: CACACAGAAACAGCTATGACC
Classes: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0068102"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 82.8%; Score 21; DB 1; Length 29;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAAATGAAA 5421
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 29

RESULT 59
A2812242 29 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0078J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0078J15 R, genomic survey sequence.

ACCESSION A2812242
VERSION A2812242.1 GI:12981296
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: J column: 15
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES
source location/Qualifiers

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0078J15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 82.8%; Score 21; DB 1; Length 29;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAAATGAAA 5421
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 29

RESULT 60
A2868731 29 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0180J02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0180J02 R, genomic survey sequence.

ACCESSION A2868731
VERSION A2868731.1 GI:13072338
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: L column: 02
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES
source location/Qualifiers

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0180J02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|9b|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5421
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 61
LOCUS TA334G090 29 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 334g09, reverse sequence,
genomic survey sequence.
ACCESSION AL491938 GI:11868238
VERSION AL491938.1
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 29)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Alkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
DIRECT SUBMISSION
SUBMITTED (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nhl@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

TITLE
JOURNAL

FEATURES

1.29
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="334g09"

Query Match 0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5421
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 62
LOCUS AG193759 29 bp DNA linear GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-071B06.T7, genomic survey
sequence.
ACCESSION AG193759
VERSION AG193759.1 GI:45225935
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

REFERENCE

1 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
BAC end sequences of library RP-43

2 (bases 1 to 29)
Unpublished

TITLE
JOURNAL
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
DIRECT SUBMISSION
SUBMITTED (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Biotechnology and Biotechnology (KRIIB), Genome Research Center (GRC),
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.kribb.re.kr, URL: <http://pms.grc.kribb.re.kr/>,
Tel: 82-42-866-7181, Fax: 82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the Red process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBAC3.6
R Site 1 : EcoRI.
R Site 2 : EcoRI.
Location/Qualifiers
1.29
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-071B06.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_11b="RP-43 Chimpanzee Male BAC library"

FEATURES

source
1.29
Location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-071B06.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_11b="RP-43 Chimpanzee Male BAC library"

Query Match 0.4%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAATGAAA 5421
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 63
LOCUS AL038650 30 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZP56611846_r1.566 (synonym: hnfcd2) Homo sapiens cDNA clone
sequence.
ACCESSION AL038650
VERSION AL038650.1 GI:49682176
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 30)
AUTHORS Ottenwelder, B., Obermayer, B., Meves, H.W., Gassenhuber, J. and

TITLE
JOURNAL
COMMENT

Wiemann,S.
EST (Otcenaeider, et al.)
Unpublished (1999)
Contact: MIRS

FEATURES
source

1. .30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKE2p5611846"
/tissue_type="Kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (gynonym: hfk42)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421
|||||
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 64

LOCUS

BG666435 30 bp mRNA linear EST 30-APR-2001
DEFINITION DRACRC02 Rat DRG Library Rattus norvegicus cDNA clone DRACRC02 5',
mRNA sequence.

ACCESSION

BG666435
BG666435.1 GI:13889357

KEYWORDS
EST.

SOURCE

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
1 (bases 1 to 30)
Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.

TITLE

Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain

Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

JOURNAL

MEDLINE

PUBMED

12060780
Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121

Email: xu.zhang@ion.ac.cn

Fax: 86-21-64713446

This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu

(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)

PCR Primers

FORWARD: T3

BACKWARD: T3

Seq primer: T3

POLYA=No.

FEATURES
source

1. .30
Location/Qualifiers

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="DRACRC02"

/sex="male"

/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421
|||||
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 65

LOCUS

BG665511 30 bp mRNA linear EST 29-MAY-2001
DEFINITION 602783643r1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4909811 5',
mRNA sequence.

ACCESSION

BG665511
BG665511.1 GI:14216051

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Unpublished (1999)
Contact: Robert Strusberg, Ph.D.
Email: c9apbs-remail.nih.gov

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLNL0809 row: e column: 12

High quality sequence stop: 30.

FEATURES

source

1. .30
Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4909811"

/clone_lib="NCI_CGAP_SG2"

/note="Organ: salivary gland; Vector: pCMV-SPORT6, Site_1:
NotI, Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Technologies. Note: this is a NCI_CGAP Library."

Technologies. Note: this is a NCI_CGAP Library."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAATGAAA 5421
|||||
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 66

LOCUS

CF280699/c 30 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H15,
mRNA sequence.

ACCESSION

CF280699
CF280699.1 GI:33658085

VERSION

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
CONTACT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)."
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--07-H15"
/cisue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAAAATGAAA 5421
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 67
CF292086 30 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--02-M10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M10, mRNA
sequence.
ACCESSION CF292086
VERSION CF292086.1 GI:33661119
SOURCE EST
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
CONTACT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)."
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--07-H15"
/cisue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

/clone="14ROOT--02-M10"
/cisue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAAAATGAAA 5421
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 68
CF299555/c 30 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-K01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K01, mRNA
sequence.
ACCESSION CF299555
VERSION CF299555.1 GI:33671316
SOURCE EST
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
CONTACT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)."
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-K01"
/cisue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAAAATGAAA 5421
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 69
CF312417/c 30 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--08-C19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

```

ABF--08-C19, mRNA sequence.
 ACCESSION CF312417
 VERSION CF312417.1 GI:33684178
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.
 FEATURES
 source
 location/Qualifiers
 1..30
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--08-C19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABP)"
 /note="vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsible
 element binding transcription factor 3 overexpression
 line."

Query Match 0.4%; Score 21; DB 1; Length 30;
 Best Local Similarity 82.8%; Pred. No. 99;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 5393 AAAAAATTCAGAAAAAGAAAAATGAAA 5421
 ||||| ||||| ||||| ||||| |||||
 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2
 RESULT 70
 LOCUS CF322226 30 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--13-M02.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--13-M02, mRNA sequence.
 ACCESSION CF322226
 VERSION CF322226
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.
 FEATURES
 source
 location/Qualifiers
 1..30
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--13-M02"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2M6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.4%; Score 21; DB 1; Length 30;
 Best Local Similarity 82.8%; Pred. No. 99;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 5393 AAAAAATTCAGAAAAAGAAAAATGAAA 5421
 ||||| ||||| ||||| ||||| |||||
 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2
 RESULT 71
 LOCUS CF327835 30 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--02-H17.g1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--02-H17, mRNA
 sequence.
 ACCESSION CF327835
 VERSION CF327835
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.
 FEATURES
 source
 location/Qualifiers
 1..30
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--02-H17"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2M6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 21; DB 1; Length 30;
 Best Local Similarity 82.8%; Pred. No. 99;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

oy	5393	AAAAAAAAATACAAAAAGAAAAAATATATAAA	5421
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	29
RESULT 72			
CP336555/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
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1..30			
/organism="Oryza sativa (japonica cultivar-group)"			
/mol type="mRNA"			
/cultivar="Nackdong"			
/db xref="taxon:39847"			
/clone="JMT--06-K13"			
/tissue type="leaf"			
/dev stage="14 days after germination"			
/lab host="E.coli DH10B"			
/clone.lib="AcJMT-overexpressing transgenic rice plasmid			
CDNA library (JMT)"			
/note="Vector: pCR4-TOPO, Site_1: EcoRI, Oligo-capped mRNA			
was reverse transcribed and then used for PCR. mRNA was			
prepared from Arabidopsis Jasmonate Carboxyl			
methyltransferase overexpression line."			
Query Match	0.4%	Score 21;	DB 1;
Best Local Similarity	82.8%	Pred. No. 99;	
Matches	24;	Conservative	0;
Mismatches			5;
Indels			0;
Gaps			0;
oy	5393	AAAAAAAAATACAAAAAGAAAAAATATATAAA	5421
Db	30	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2
RESULT 73			
CNS45845/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
1..30			
/organism="Oryza sativa (japonica cultivar-group)"			
/mol type="mRNA"			
/cultivar="Nackdong"			
/db xref="taxon:39847"			
/clone="JMT--06-K13"			
/tissue type="leaf"			
/dev stage="14 days after germination"			
/lab host="E.coli DH10B"			
/clone.lib="AcJMT-overexpressing transgenic rice plasmid			
CDNA library (JMT)"			
/note="Vector: pCR4-TOPO, Site_1: EcoRI, Oligo-capped mRNA			
was reverse transcribed and then used for PCR. mRNA was			
prepared from Arabidopsis Jasmonate Carboxyl			
methyltransferase overexpression line."			
Query Match	0.4%	Score 21;	DB 1;
Best Local Similarity	82.8%	Pred. No. 99;	
Matches	24;	Conservative	0;
Mismatches			5;
Indels			0;
Gaps			0;
oy	5393	AAAAAAAAATACAAAAAGAAAAAATATATAAA	5421
Db	30	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2
RESULT 73			
CNS45845/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
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1..30			
/organism="Oryza sativa (japonica cultivar-group)"			
/mol type="mRNA"			
/cultivar="Nackdong"			
/db xref="taxon:39847"			
/clone="JMT--06-K13"			
/tissue type="leaf"			
/dev stage="14 days after germination"			
/lab host="E.coli DH10B"			
/clone.lib="AcJMT-overexpressing transgenic rice plasmid			
CDNA library (JMT)"			
/note="Vector: pCR4-TOPO, Site_1: EcoRI, Oligo-capped mRNA			
was reverse transcribed and then used for PCR. mRNA was			
prepared from Arabidopsis Jasmonate Carboxyl			
methyltransferase overexpression line."			
Query Match	0.4%	Score 21;	DB 1;
Best Local Similarity	82.8%	Pred. No. 99;	
Matches	24;	Conservative	0;
Mismatches			5;
Indels			0;
Gaps			0;
oy	5393	AAAAAAAAATACAAAAAGAAAAAATATATAAA	5421
Db	30	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2
RESULT 73			
CNS45845/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
1..30			
/organism="Oryza sativa (japonica cultivar-group)"			
/mol type="mRNA"			

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TITLE
Hamdi,S., Romieu,C. and Textier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Université de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
SOURCE
1. .30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/cclone="B3CS00RL002E09"
/dev_stage="ripening stage"
/cclone_1lb="Ripe Grape Skin Triplex2 Library"
/ncote="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
5f1A; Site_2: 5f1B; Oriented library"

Qy 5393 AAAAAAAAAAGAAAAATGAAA 5421
Db 29 AAAAAAAAAAAAAAAAAAAAAA 1

Query Match 0.44; Score 21; DB 1; Length 30;
Best local similarity 82.84; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 74
CN545913/c 30 bp mRNA linear EST 30-APR-2004
LOCUS
CN545913
DEFINITION
EST 17857 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL006C10 3', mRNA sequence.
ACCESSION
CN545913
VERSION
CN545913.1 GI:46910538
KEYWORDS
EST.
ORGANISM
Vitis vinifera
Vitis vinifera
Bkaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Textier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
SOURCE
1. .30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/cclone="B3CS00RL006C10"
/dev_stage="ripening stage"

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/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiIB; Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAATGAAAA 5421
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 75
CN546459/c 30 bp mRNA linear EST 30-APR-2004
LOCUS EST 18603 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
ACCESSION CN546459
VERSION CN546459.1 GI:46911084
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Komieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007C01"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAATGAAAA 5421
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 76
CN546474/c 30 bp mRNA linear EST 30-APR-2004
LOCUS EST 18618 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION CDNA clone B3CS57RB007D06 3', mRNA sequence.
ACCESSION CN546474
VERSION CN546474.1 GI:46911099
KEYWORDS EST.
SOURCE Vitis vinifera

ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Komieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007D06"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAATGAAAA 5421
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 77
CN546789/c 30 bp mRNA linear EST 30-APR-2004
LOCUS EST 18560 Turning Grape Berry Lambda Triplex2 Library Vitis
DEFINITION vinifera CDNA clone B3CS38TB008G04 3', mRNA sequence.
ACCESSION CN546789
VERSION CN546789.1 GI:46915099
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Komieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source Location/Qualifiers

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source
1. .30
/organism="Vitis vinifera"
/mol_type="RNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS18T08G04"
/dev_stage="viralson stage"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SflIA; Site_2: SflIB; Oriented library"

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAATGAAA 5421
DB 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 78
LOCUS AZ357603 30 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0099H17P Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0099H17 F, genomic survey sequence.
ACCESSION AZ357603
VERSION AZ357603.1 GI:10471303
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhuesern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: H column: 17
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0099H17"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-."
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to

```

```

10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (GI:4732114|gb|AF29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAATGAAA 5421
DB 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 79
LOCUS AZ455741 30 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0258D16F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0258D16 F, genomic survey sequence.
ACCESSION AZ455741
VERSION AZ455741.1 GI:10613866
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhuesern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: D column: 16
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0258D16"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-."
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

```


electroporesis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAATGAAA 5421
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 29

RESULT 80
AZ481739/c 30 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0306N12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0306N12 F, genomic survey sequence.

ACCESSION AZ481739
VERSION AZ481739.1 GI:10642804
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: N column: 12
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES

source

1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0306N12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAATGAAA 5421
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 81
AZ582114/c 30 bp DNA linear GSS 13-DEC-2000
LOCUS AZ582114/c
DEFINITION 1M0374U17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0374U17 F, genomic survey sequence.

ACCESSION AZ582114
VERSION AZ582114.1 GI:11700674
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0374 row: J column: 17
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES

source

1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0374U17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAAATGAAA 5421
Db 30 AAAAAAAAAAAGAAAAATGAAA 2

RESULT 82
AG191161 30 bp DNA linear GSS 06-MAR-2004
LOCUS AG191161
DEFINITION Pan troglodytes DNA, clone: RP43-066P20.T7, genomic survey
sequence.
ACCESSION AG191161 GI:45223337
VERSION AG191161.1
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE BAC end sequences of library RP-43
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 30)
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE Direct Submision
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
BioScience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.krribb.re.kr, URL:http://pns.grc.krribb.re.kr/;
Tel:82-42-866-7181, Fax:82-42-860-4409)

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the RAD process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7

LIBRARY
Vector : pBACe3.6
R.Site 1 : EcorI
R.Site 2 : EcorI.
Location/Qualifiers
1. 30

/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-066P20.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC library"

Query Match 0.4%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 99;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAAAATGAAA 5421
Db 30 AAAAAAAAAAAGAAAAATGAAA 2

RESULT 83
AU267990/c 29 bp mRNA linear EST 26-APR-2004
LOCUS AU267990

DEFINITION AU267990 VS Dictyostelium discoideum cDNA clone VSH801 5', mRNA
sequence.

ACCESSION AU267990
VERSION AU267990.1 GI:20526788
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum

REFERENCE 1
AUTHORS Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
1 (bases 1 to 29)

TITLE Maeda, M., Williams, J.G., Takeuchi, I. and Tanaka, Y.
JOURNAL Analyses of cDNAs from growth and slug stages of Dictyostelium
discoideum
CONTACT: Nucleic Acids Res. 32 (5), 1647-1653 (2004)
Contract: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hidekobio@tsukuba.ac.jp.

FEATURES
source
Location/Qualifiers
1. 29

/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH801"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.4%; Score 20.8; DB 1; Length 29;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5391 TTTAAAAATACAAAAAGAAAA 5414
Db 29 TTTAAAAATACAAAAAGAAAA 6

RESULT 84
AZ941721/c 27 bp DNA linear GSS 26-APR-2001
LOCUS 2M0201004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION Clons UUGC2M0201004 R, genomic survey sequence.
ACCESSION AZ941721
VERSION AZ941721
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)

TITLE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
JOURNAL Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
COMMENT Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Inset: 0201 row: 0 column: 04
Seq primer: CACACGAAACACGCTATGACC
Class: plasmid ends

FEATURES
source
High quality sequence stop: 27.
Location/Qualifiers

1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0201004"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 20.6; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 99;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5394 AAAAAATACAAAAGAAAAATGAA 5420
|||||
Db 27 AAAAAAAAAAAAAAAAAAGAAA 1

RESULT 85
A2970621/c 27 bp DNA linear GSS 27-APR-2001
LOCUS 2M0243N14R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
DEFINITION clone UUCG2M0243N14 R, genomic survey sequence.
ACCESSION A2970621
VERSION A2970621.1 GI:13841848
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Haml,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0243 row: N column: 14
Seq primer: CACACAGGAACGCTATGACC
Classes: plasmid ends
High quality sequence stop: 27.

FEATURES
source
Location/Qualifiers

1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0243N14"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 20.6; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 99;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAGAAAAATGAA 5419
|||||
Db 27 AAAAAAAAAAAAAAAAAAGAA 1

RESULT 86
CF307749/c 28 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--01-E17.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--01-E17, mRNA sequence.
ACCESSION CF307749
VERSION CF307749.1 GI:33679510
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE
AUTHORS Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eupharbioidae; Oryzaceae; Oryza.

JOURNAL
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers

1..28
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--01-E17"
/tissue_type="leaf"

/dev stage="14 days after germination"
 /lab host="E.coli DH10B"
 /clone lib="ABP3-overexpressing transgenic rice plasmid
 cDNA library (ABP)"
 /note="Vector: pCR4-TOPO, Site_1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.4%; Score 20.6; DB 1; Length 28;
 Best Local Similarity 85.2%; Pred. No. 1e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5395 AAAAAATACAAAAAGAAAAATGAAAA 5421
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 87
 AZ824574/c 28 bp DNA linear GSS 20-FRB-2001
 LOCUS 2M0099D17P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

SS.
 Mus musculus (house mouse)

ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: D column: 17
 Seq primer: CCGTGTAAACACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0099D17"
 /sex="Male"
 /lab host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel

FEATURES
 source

electroporesis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.4%; Score 20.6; DB 1; Length 28;
 Best Local Similarity 85.2%; Pred. No. 1e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5395 AAAAAATACAAAAAGAAAAATGAAAA 5421
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 88
 AZ836072/c 28 bp DNA linear GSS 20-FRB-2001
 LOCUS 2M0130K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

SS.
 Mus musculus (house mouse)

ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0130 row: K column: 08
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0130K08"
 /sex="Male"
 /lab host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel

FEATURES
 source

electroporesis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 20.6; DB 1; Length 28;
Best Local Similarity 85.2%; Pred. No. 1e+02; 4; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5394 AAAAAAAAAAAGAAAAATGAA 5420
Db 28 AAAAAAAAAAAGAAAAATGAA 2

RESULT 89
LOCUS BQ583967/c
DEFINITION S013297-024-004-B01-T7 MP1Z-ADIS-024-inflorescence Beta vulgaris
ACCESSION BQ583967
VERSION BQ583967.1 GI:26113544
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 29)

Hewig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wuck, W., Menze, A., O'Brien, J., Lebrach, H. and Radloff, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)
22362189
12472698

COMMENT Contact: Weishaar B

ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weishaar@mp1z-koeln.mpg.de

Insert length: 29 Std Error: 0.00

Place: 4 row: B column: 01

Seq primer: T7; GTAATACGACTCTACTATAGGC.

Location/Qualifiers

FEATURES

source

1..29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:182728"
/db_xref="taxon:161934"
/clone="024-004-B01"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_11b="MP1Z-ADIS-024-inflorescence"
/note="Vector: PCWVSPORE; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanleberener Saatgut AG Binbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.4%; Score 20.6; DB 1; Length 29;
Best Local Similarity 85.2%; Pred. No. 1.1e+02;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5393 AAAAAAAAAAAGAAAAATGAA 5419
Db 27 AAAAAAAAAAAGAAAAATGAA 1

RESULT 90
LOCUS CF317007/c
DEFINITION HD--06-114.g1 OsHDA1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION CF317007
VERSION CF317007.1 GI:33688768
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 25)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_11b="OsHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice histone Deacetylase overexpression line."

Query Match 0.4%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1e+02; 3; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAAAAATACAAAAAAGAAAAA 5415
Db 25 TTTAAAAAATACAAAAAAGAAAAA 1

RESULT 91
LOCUS AL038686
DEFINITION DKFZP566J0546_r1 566 (synonym: hfkcd2) Homo sapiens cDNA clone
ACCESSION AL038686
VERSION AL038686.1 GI:49682186
KEYWORDS EST.
SOURCE Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 26)

AUTHORS Ootemwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
 TITLE EST (Ootemwaelder, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS

FEATURES
 source Ingoltseder Landstr.1, D-85764 Neuherberg, Germany.
 Location/Qualifiers

1.26
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZ565J0546"
 /tissue_type="kidney"
 /dev_stage="fetal"
 /lab_host="X1-2D1ue"
 /clone_1ib="566 (synonym: hfkcd2)"
 /note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.4%; Score 20.2; DB 1; Length 26;
 Best Local Similarity 88.0%; Pred. No. 1.1e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAATAATACAAAAAGAAAAA 5415
 Db 1 TTTAAAAAAAAAAAAAAAAAAAAA 25

RESULT 92
 CF299646/c 26 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--03-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L24, mRNA
 sequence.

ACCESSION CF299646 GI:33671407
 VERSION CF299646
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.T., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC., DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYONGGI, KOREA
 TEL: 82 31 321 6355
 FAX: 82 31 321 6355
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1.26
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI, mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.4%; Score 20.2; DB 1; Length 26;
 Best Local Similarity 88.0%; Pred. No. 1.1e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5390 ATTAAAAATACAAAAAGAAAAA 5414
 Db 25 ATTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 93
 CF337400 28 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--07-N04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--07-N04, mRNA sequence.

ACCESSION CF337400 GI:33823200
 VERSION CF337400
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 28)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.T., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC., DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYONGGI, KOREA
 TEL: 82 31 321 6355
 FAX: 82 31 321 6355
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1.28
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--07-N04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1ib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jaominate Carboxyl
 methyltransferase overexpression line."

Query Match 0.4%; Score 20.2; DB 1; Length 28;
 Best Local Similarity 88.0%; Pred. No. 1.2e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAAAATACAAAAAGAAAAA 5415
 Db 1 TTTAAAAAAAAAAAAAAAAAAAAA 25

RESULT 94
 A1971979 28 bp mRNA linear EST 27-OCT-1999
 LOCUS WV30h06.x1 NCI CGAP Ovis 18 Homo sapiens cDNA clone IMAGE:2531099.3,
 DEFINITION similar to TR063545 O63545 NMDH DEHYDROGENASE SUBUNIT 5; contains
 TARI.b1 TARI repetitive element 1, mRNA sequence.

ACCESSION A1971979 GI:5768805
 VERSION A1971979
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 28)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c99abs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento
Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
www.bio.lnlni.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
location/Qualifiers
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2531099"
/tissue_type="fibrothecoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
/note="Organ: ovary; Vector: pYT73D-Pac (pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCATCTGAGTGGAGCGCGCGACATTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pYT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Patricia Bonaldo. "

Query Match 0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5386 AAGAAATTAATAAATACAAAAAGAAA 5413
Db 1 AAGAAAAAACAAACAAACAAAGAACCA 28

RESULT 95
AJ666435/c
LOCUS
DEFINITION AJ666435 CSEQRAN09 Sus scrofa CDNA clone C0000033_L21, mRNA
ACCESSION
VERSION AJ666435
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 28)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector: BluescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Location/Qualifiers

source

1..28
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_L21"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match 0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAAAGAAAAATGAAA 5420
Db 28 AAAAAAATAAATAAATAAATAAATAA 1

RESULT 96
AM332443/c
LOCUS
DEFINITION AM332443 28 bp mRNA linear EST 31-JAN-2000
ACCESSION
VERSION AM332443.1 GI:6828800
KEYWORDS
SOURCE
ORGANISM
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 28)
Smilian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers

FEATURES
source
1..28
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Tritox extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/

Query Match 0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAAAGAAAAATGAAA 5420
Db 28 AAAAAAATAAATAAATAAATAAATAA 1

RESULT 97
CF282351/c
LOCUS
DEFINITION CF282351 28 bp mRNA linear EST 14-AUG-2003
14ETL--09-N05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (Japonica cultivar-group) CDNA clone 14ETL--09-N05,
mRNA sequence.


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ACCESSION   CF282351
VERSION     CF282351.1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomic and Genetic Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..28
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="HD-13-E16"
            /issue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_1lb="Rice etiolated leaf plasmid cDNA library
            (14E1L)"
            /note="Vector: pCR4-TOPO, Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAGAAATGAAA 5420
    |||||
    28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 98
CF321885      28 bp      mRNA      linear      EST 15-AUG-2003
HD-13-E16.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD-13-E16, mRNA sequence.

ACCESSION   CF321885
VERSION     CF321885.1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomic and Genetic Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="NACL-06-014"
            /issue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_1lb="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: pCR4-TOPO, Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-13-E16"
/issue_type="callus"
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/lab_host="E.coli DH10B"
/clone_1lb="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO, Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAGAAATGAAA 5420
    |||||
    28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 99
CF330748      28 bp      mRNA      linear      EST 18-AUG-2003
NACL-06-014.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL-06-014, mRNA
sequence.

ACCESSION   CF330748
VERSION     CF330748.1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomic and Genetic Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="NACL-06-014"
            /issue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_1lb="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: pCR4-TOPO, Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAGAAATGAAA 5420
    |||||
    28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 100
CF330938      28 bp      mRNA      linear      EST 18-ANG-2003
LOCUS        NACL--06-N19.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION   sativa (japónica cultivar-group) cDNA clone NACL--06-N19, mRNA
sequence.
ACCESSION    CF330938
VERSION      CF330938
KEYWORDS     EST.
SOURCE       Oryza sativa (japónica cultivar-group)
ORGANISM     Oryza sativa (japónica cultivar-group)
REFERENCE    1 (bases 1 to 28)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
JOURNAL      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc., Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
              1..28
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               /cultivar="Nackdong"
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               /clone="NACL--06-N19"
               /tissue_type="callus"
               /dev_stage="proliferated callus on 2N6 media for 30 days"
               /lab_host="E.coli DH10B"
               /clone_1lb="Rice callus plasmid cDNA library (NACL)"
               /note="Vector: PCR4-TOPO, Site_1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."
Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAACAAAAAGAAAAATGAAA 5420
        ||||| ||||| ||||| ||||| |||||
        1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 101
CN546364      28 bp      mRNA      linear      EST 30-APR-2004
LOCUS        EST 18317 Green Grape Berry Lambda Triplex2 library Vitis vinifera
DEFINITION   cDNA clone B3CS1XGB016C01 3', mRNA sequence.
ACCESSION    CN546364
VERSION      CN546364.1 GI:46910989
KEYWORDS     EST.
SOURCE       Vitis vinifera
ORGANISM     Vitis vinifera
REFERENCE    1 (bases 1 to 28)
AUTHORS      Abbal,P., Agasee,A., Ageorges,A., Atanasova,R., Barrieu,F.,
              Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
              Hamdi,S., Romieu,C. and Terrier,N.
              Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
              or seeds) at Various Developmental Stages
              Unpublished (2002)
JOURNAL      Contact: Hamdi S.
COMMENT      Contact: Hamdi S.

```

```

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.
FEATURES     Location/Qualifiers
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               /organism="Vitis vinifera"
               /mol_type="mRNA"
               /cultivar="Cabernet Sauvignon"
               /db_xref="taxon:29760"
               /clone="B3CS37TB007H02"
               /dev_stage="veraison stage"
               /clone_1lb="Green Grape Berry Lambda Triplex2 library"
               /note="Organ: Fruit without seeds; Vector: Lambda
               Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAACAAAAAGAAAAATGAAA 5420
        ||||| ||||| ||||| ||||| |||||
        28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 102
CN546703      28 bp      mRNA      linear      EST 30-APR-2004
LOCUS        CN546703/c
DEFINITION   EST 18474 Turning Grape Berry Lambda Triplex2 library Vitis
vinifera cDNA clone B3CS37TB007H02 3', mRNA sequence.
ACCESSION    CN546703
VERSION      CN546703.1 GI:46911328
KEYWORDS     EST.
SOURCE       Vitis vinifera
ORGANISM     Vitis vinifera
REFERENCE    1 (bases 1 to 28)
AUTHORS      Abbal,P., Agasee,A., Ageorges,A., Atanasova,R., Barrieu,F.,
              Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
              Hamdi,S., Romieu,C. and Terrier,N.
              Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
              or seeds) at Various Developmental Stages
              Unpublished (2002)
JOURNAL      Contact: Hamdi S.
COMMENT      UMR 619 - Equipe Biologie de la Vigne
              Universite de Bordeaux I, Institut National de la Recherche
              Agronomique
              71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
              France
              Tel: 00-33-(0)5-57-12-25-50
              Fax: 00-33-(0)5-57-12-25-48
              Email: s.hamdi@bordeaux.inra.fr
              Seq primer: 17.
FEATURES     Location/Qualifiers
              1..28
               /organism="Vitis vinifera"
               /mol_type="mRNA"
               /cultivar="Cabernet Sauvignon"
               /db_xref="taxon:29760"
               /clone="B3CS37TB007H02"
               /dev_stage="veraison stage"
               /clone_1lb="Turning Grape Berry Lambda Triplex2 library"
               /note="Organ: Fruit without seeds; Vector: Lambda
               Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match      0.4%; Score 20; DB 1; Length 28;

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Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAAATGAA 5420
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 103

AZ399637 28 bp DNA linear GSS 03-OCT-2000
LOCUS AZ399637/c
DEFINITION 1M0165N04R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0165N04 R, genomic survey sequence.

ACCESSION AZ399637
VERSION AZ399637.1 GI:10514711

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)

REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: N column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers

FEATURES

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0165N04"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42ny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAAATGAA 5420
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 104

AZ401766 28 bp DNA linear GSS 03-OCT-2000
LOCUS AZ401766
DEFINITION 1M0168008R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0168008 R, genomic survey sequence.

ACCESSION AZ401766
VERSION AZ401766.1 GI:10516840

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)

REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: O column: 08
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers

FEATURES

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0168008"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42ny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

D_b 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 107	LOCUS	DEFINITION
AZ653365/c	AZ653365	28 bp DNA linear GSS 14-DEC-2000
	1M0527B02P	Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0527B02 P, genomic survey sequence.

VERSION AZ653365.1 GI:11790511

SOURCE ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCES
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamll, C.,
1 (pages 1 to 28)
Eukaryotes; Metazoa; Chordata; Crustacea; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B.

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Email: ddunn@genetics.wash.edu
Insert Length: 10000 Std Error: 0.000
Plate: 0527 row: B column: 02
Seq primer: CCGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

source	1. .28
--------	--------

FEATURES
Source

FEATURES	Location/Qualifiers
SOURCE	1. .28

FEATURES	Location/Qualifiers
Source	1. .28

Db

28 AAAAAAAAAAAAAAAAAAAAAA I

RESULT	LOCUS	DEFINITION
108 AZ785035/C	AZ785035	28 bp DNA linear GSS 16-FEB-2001
	2M002BJ01R	Mouse 10kb plasmid tUGC1M library Mus musculus genomic clone tUGC2M002BJ01 R, genomic survey sequence.

VERSION AZ785035.1 GI:12921373

SOURCE ORGANISM	Mus musculus (house mouse)
Mus musculus	

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Hamil, C.,
1 (bases 1 to 28)

TITLE Mouse whole genome scaffolding with paired end reads from 10kbp

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0028 row: J column: 01
Seq primer: CACACGGAACACGCTATGCACC
Class: plasmid ends
High quality sequence stop: 28.

Source	1. .28
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Query Match	0.4;	Score 20;	DB 1;	Length 28;
Best Local Similarity	82.1;	Pred. No. 1.2e+02;		
Matches 23;	Conservative	5;	Mismatches	0;
			Indels	0;
			Gaps	0;

5393 AAAAAATACAAAAGAAAATGAA 5420

Query Match 0.48; Score 20; DB 1; Length 28.

Matches	23;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
5393	AAAAAAAAATACAAAAAGAAAAATGAAA	5420							

Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 109
AZ824519/c      28 bp   DNA      linear   GSS 20-FEB-2001
LOCUS          AZ824519
DEFINITION     2M009109F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M009109 F, genomic survey sequence.
ACCESSION      AZ824519
VERSION        AZ824519.1 GI:12994427
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Reilly,M., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE          Unpublished (2000)
JOURNAL        Contract: Robert B. Weiss
COMMENT        University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0099 row: 1 column: 09
               Seq primer: CGTTGTAACGACGCGCCAGT
               Class: plasmid ends
               High quality sequence stop: 28.
FEATURES       location/Qualifiers
               1..28
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC2M009109"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
               /clone_1lb="Mouse 10kb plasmid UUGC1M library"
               /note="Vector: PMD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adapted DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAACAAAAAGAAAAATGAAA 5420
    ||||| ||||| ||||| ||||| |||||
DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 110
AZ833425
LOCUS          AZ833425
DEFINITION     2M0115D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0115D04 R, genomic survey sequence.
ACCESSION      AZ833425
VERSION        AZ833425.1 GI:13003333
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Reilly,M., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE          Unpublished (2000)
JOURNAL        Contract: Robert B. Weiss
COMMENT        University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0115 row: D column: 04
               Seq primer: CACACGAAACAGCTATGACC
               Class: plasmid ends
               High quality sequence stop: 28.
FEATURES       location/Qualifiers
               1..28
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC2M0115D04"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
               /clone_1lb="Mouse 10kb plasmid UUGC1M library"
               /note="Vector: PMD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adapted DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
Query Match      0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAACAAAAAGAAAAATGAAA 5420
    ||||| ||||| ||||| ||||| |||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

```

RESULT 111
 AZ866569/c
 LOCUS 28 bp DNA linear GSS 21-FEB-2001
 DEFINITION 2M0177B08F Mouse 10kb plasmid UGCGM library Mus musculus genomic
 accession
 AZ866569
 version UGCGM0177B08 F, genomic survey sequence.
 accession
 AZ866569.1 GI:13068007
 keywords
 GSS.
 source
 Mus musculus (house mouse)
 organism
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
 Iselm,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0177 Row: B Column: 08
 Seq primer: CGTTGTAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0177B08"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD29v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI:4732114|db|AF12072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent R. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.4%; Score 20; DB 1; Length 28;
 Best Local Similarity 82.1%; Pred. No. 1.2e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 5393 AAAAAATACAAAAAGAAAAATGAAA 5420
 ||||| ||||| ||||| ||||| |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 112

TA291A01Q
 LOCUS 28 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 291a01, reverse sequence,
 genomic survey sequence.
 accession
 AL486613
 version AL486613.1 GI:11853602
 keywords
 GSS.
 source
 Trypanosoma brucei
 Trypanosoma brucei
 organism
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 28)
 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 Direct Submision
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..28
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="291a01"

Query Match 0.4%; Score 20; DB 1; Length 28;
 Best Local Similarity 82.1%; Pred. No. 1.2e+02;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 5393 AAAAAATACAAAAAGAAAAATGAAA 5420
 ||||| ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 113
 TA29A09P/c
 LOCUS 28 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 29a09, forward sequence,
 genomic survey sequence.
 accession
 AL453073
 version AL453073.1 GI:11854584
 keywords
 GSS.
 source
 Trypanosoma brucei
 Trypanosoma brucei
 organism
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 28)
 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 Direct Submision
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="29a09"

Query Match 0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5398 AATACAAAGAAAAATGAAATPAA 5425
DB 28 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 114

TA379D1P/C

LOCUS TA379D1P 28 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 379d11, forward sequence,
genomic survey sequence.

ACCESSION AL497637

VERSION AL497637.1 GI:11873359

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM

Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 28)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., Bl-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

TITLE

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="379d11"

Query Match 0.4%; Score 20; DB 1; Length 28;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAATGAAA 5420
||||| ||||| ||||| ||||| |||||

DB 28 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 115

BG929133/C

LOCUS HNC34-1-B8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION HNC34-1-B8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

ACCESSION BG929133

VERSION BG929133.1 GI:14323656

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 25)

Kumar S., Connor, J.R., Dadds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Satche, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.

Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritis cartilage cDNA libraries
Osteoarthritis. Cartil. 9 (7), 641-653 (2001)

JOURNAL 21482651

MEDLINE 11597177

PUBMED

COMMENT

Contract: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@sk.com
Seq primer: 17.

FEATURES

source

1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_id="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
directional"

Query Match 0.4%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAAAAATGAAA 5415
DB 25 AAAAAAAAAACATTAAGAAAAA 3
||||| ||||| ||||| ||||| |||||

RESULT 116

CD028815

LOCUS CD028815 27 bp mRNA linear EST 07-MAY-2003
DEFINITION mgc8010xA10f.b Magnaporthe grisea CS Uni-Zag XR Library Magnaporthe
grisea cDNA clone mgc8010xA10 5', mRNA sequence.

ACCESSION CD028815

VERSION CD028815.1 GI:30410271

KEYWORDS EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM

Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 27)

Ebbole, D.D., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatterai, K. and Dean, R.A.

Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
Unpublished (2002)

JOURNAL Unpublished (2002)
CONTACT: Ebbole DU
DEPARTMENT: Plant Pathology & Microbiology

Texas A&M University
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
 Tel: 979 845 4831
 Fax: 979 845 6483
 Email: d-ebold@tamu.edu
 Chromatogram file of this sequence is available, see contact person;

PCR Primers
 FORWARD: T3 primer
 BACKWARD: T7 primer
 Plate: mgc010 row: A column: 10
 Seq primer: T3.

FEATURES

source

1. .27
 /organism="Magnetorthe grisea"
 /mol_type="rRNA"
 /strain="Guy11"
 /db_xref="taxon:148305"
 /clone="mgc010x10"
 /sex="Mat1-2 hermaphrodite"
 /cell_type="conidia"
 /clone_lib="Magnetorthe grisea CS Uni-Zap XR library"
 /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI site of insert. Confidial library. Point inoculation of Guy11 at center of oatmeal agar plate. Conidia were harvested after two weeks of growth. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

Query Match 0.4%; Score 19.8; DB 1; Length 27;
 Best Local Similarity 91.3%; Pred. No. 1.2e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAAATC 1202
 |||||
 Db 3 AGAGAGAGAGAGAGAGAACTC 25

RESULT 117
 CL654516 27 bp DNA linear GSS 09-JUL-2004
 LOCUS PR10120d_B08 - PR10120d_B21 (27) Note: Recurring String Mixed stage
 DEFINITION fosmid library of P. pacificus var. California Pterionchus
 pacificus genomic, genomic survey sequence.

ACCESSION CL654516 GI:50133465
 VERSION
 KEYWORDS
 SOURCE Pterionchus pacificus
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pterionchus.

REFERENCE 1 (bases 1 to 27)
 Sriinivasan,J., Otto,G.W., Kahlw,U., Geisler,R. and Sommer,R.J.
 ApplDB: an AcceDB database for the nematode satellite organism
 Pterionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 CONTACT: Sommer RJ

JOURNAL

COMMENT

Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.

FEATURES

Location/Qualifiers

source

1. .27
 /organism="Pterionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pBf105-5 Fosmid vector"

Query Match 0.4%; Score 19.8; DB 1; Length 27;
 Best Local Similarity 91.3%; Pred. No. 1.2e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATCAAAAAAGAAAAA 5415
 |||||
 Db 23 AAAAAATCAAAAAAGAAAAA 1

RESULT 118
 A2776487 27 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0010G08F Mouse 10kb plasmid UGCGM library Mus musculus genomic
 DEFINITION clone UGCG2M0010G08 F, genomic survey sequence.

ACCESSION A2776487
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM

REFERENCE 1 (bases 1 to 27)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Iselm,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
 Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weisb,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT Contact: Robert B. Weise
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0010 row: G column: 08
 Seq primer: CGTGTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES

source

1. .27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0010G08"
 /sex="Male"
 /lab_host="G. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD22uv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adapter oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1181 GAGAAAGAGAGAGAGAAATCAGAG 1206
Db 2 GAGAGAGAGAGAGAGAGAGAGAG 27

RESULT 119
AZ862643/c 27 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0170U19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0170U19 F, genomic survey sequence.
ACCESSION AZ862643
VERSION AZ862643.1 GI:13060151
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)
SOURCE Mus musculus

REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0170 row: J column: 19
Seq primer: CCGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES
source 1..27

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0170U19"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5393 AAAAATTCAAAAAGAAAATGA 5418
Db 26 AAAAAAAAAAAAAAAAAAAAAAAGA 1

RESULT 120
AZ873739/c 27 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0187C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0187C08 R, genomic survey sequence.
ACCESSION AZ873739
VERSION AZ873739.1 GI:13082111
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)
SOURCE Mus musculus

REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0187 row: C column: 08
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES
source 1..27

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0187C08"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1173 AGAATCAGAAAGAGAGAGAGA 1198
Db 27 AGAGCTTAGAGAGAGAGAGAGA 2

RESULT 121
TA257B07P 27 bp DNA 1linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 257b07, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL483278.1 GI:11849602
VERSION AL483278.1 GI:11849602
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 27)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Subcloning
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Genome Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhls@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nhlsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source location/Qualifiers

1..27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="257b07"

Query Match 0.4%; Score 19.6; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5395 AAAAAATACAAAAAGAAAAATGAAA 5421
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 122
AZ430288/c 23 bp DNA 1linear GSS 03-OCT-2000
LOCUS 1M0214012R Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0214012 R, genomic survey sequence.
ACCESSION AZ430288
VERSION AZ430288.1 GI:10554301
KEYWORDS GSS.

SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00
Plate: 0214 row: O column: 12
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0214012"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: pMD42uv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1180 AGAGAAAGAGAGAGAGAAA 1200
Db 23 AGAGAGAGAGAGAGAGAGAAA 3

RESULT 123
AL587648 25 bp mRNA 1linear EST 02-MAR-2001
LOCUS AL587648 BP Chicken Brain Library Gallus gallus cDNA clone
DEFINITION ROS060C07, mRNA sequence.
ACCESSION AL587648
VERSION AL587648.1 GI:13192682
KEYWORDS EST.
SOURCE Gallus gallus (chicken)

ORGANISM

Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianine; Gallus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 25)

Murray, F.

BP Chicken Brain Library

Unpublished (2001)

Contact: Frazer Murray

Dept. Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@bbsrc.ac.uk

GCAGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech

(*6854-

Seq primer: M13P.

FEATURES

source

Location/Qualifiers

1..25

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="ROS060C07"

/tissue_type="Brain"

/dev_stage="Unknown"

/lab_host="DH10B"

/clone_lib="BP Chicken Brain Library"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned

unidirectionally. Primer: Oligo dt. 5' adaptor sequence:

5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'

CGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from

Clontech (*6854-1)"

Query Match 0.4%; Score 19.2; DB 1; Length 25;

Best Local Similarity 87.5%; Pred. No. 1.4e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAAT 5416

Db 24 AAAAAAAAAAAAAAAAAAAAAAT 1

RESULT 124

LOCUS

DEFINITION

AZ381039 25 bp DNA linear GSS 02-OCT-2000

1M0137N18F Mouse 10kb plasmid UUC1M library Mus musculus genomic

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

FEATURES

source

Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

1..25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0137N18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male); Was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (g14732114[gbl]AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.4%; Score 19.2; DB 1; Length 25;

Best Local Similarity 87.5%; Pred. No. 1.4e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAAT 5416

Db 2 AAAAAAAAAAAAAAAAAAAAAAT 25

RESULT 125

LOCUS

DEFINITION

AZ386891 25 bp DNA linear GSS 02-OCT-2000

1M0146A08F Mouse 10kb plasmid UUC1M library Mus musculus genomic

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

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JOURNAL

COMMENT

Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

1.25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MUC1M0146N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M1 library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5393 AAAAAAAAAACAAAAAGAAAAAT 5416
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAT 24

RESULT 126
LOCUS AL587774/c 26 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587774 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION AL587774
VERSION AL587774.1 GI:13192808
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 26)
Murray P.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGCCGCTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech (*6854-
Seq primer: M13P.
FEATURES
Location/Qualifiers
1..26
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"

/clone="ROS063A11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_1lb="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

Query Match 0.4%; Score 19.2; DB 1; Length 26;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5393 AAAAAAAAAACAAAAAGAAAAAT 5416
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAT 1

RESULT 127
LOCUS R26779/c 26 bp mRNA linear EST 24-APR-1995
DEFINITION yh44f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:132611 3' similar to gb|W85164 SERIN RESPONSE FACTOR ACSSSORV PROTEIN 1A (HUMAN);, mRNA sequence.
ACCESSION R26779
VERSION R26779.1 GI:782914
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 26)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, B., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The Washu-Mercer EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1384
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LBNL
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1384 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..26
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:538233"
/db_xref="taxon:9606"
/clone="IMAGE:132611"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_1lb="Soares placenta Nb2HP"
/note="Organ: placenta; Vector: pRTT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGATTCGCGCCGCGAGCAATTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors

TITLE The Washu-Mercer EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1384
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LBNL
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1384 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..26
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:538233"
/db_xref="taxon:9606"
/clone="IMAGE:132611"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_1lb="Soares placenta Nb2HP"
/note="Organ: placenta; Vector: pRTT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGATTCGCGCCGCGAGCAATTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors

(pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatma Bonaldo. "

Query Match 0.4%; Score 19.2; DB 1; Length 26;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5391 TTTAAAAAATACAAAAAGAAAA 5414
Db 24 TTTAAAAAATACAAAAAGAAAA 1

RESULT 128

LOCUS AM327923 27 bp mRNA linear EST 28-JAN-2000
DEFINITION dr02g08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA sequence.

ACCESSION AM327923
VERSION AM327923.1 GI:6798418
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 27)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgaabs-remail.nih.gov
COMMENT Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Edge Biosystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: www.bio.liml.gov/bbrp/image/image.html

Plate: L1CM0029 row: M column: 16
Seq primer: -21M13 forward primer (AB1).

FEATURES
source Location/Qualifiers

1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2847159"
/tissue_type="Burkitt lymphoma"
/cell_line="MGC4"
/clone_lib="NIH MGC_3"
/note="Organ: Lymph; Vector: pOTB7a; Library prepared by Edge Biosystems."

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAA 5415
Db 1 AAAAAAATACAAAAAGAAAA 27

RESULT 129
LOCUS CF291968/c 27 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-J21, mRNA sequence.

ACCESSION CF291968
VERSION CF291968.1 GI:33661001
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Emaritoidae; Oryzae; Oryza. 1 (bases 1 to 27)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
JOURNAL Contact: Nahm B.H.
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-J21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAA 5415
Db 27 AAAAAAATACAAAAAGAAAA 1

RESULT 130

LOCUS CF328811/c 27 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-009.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-009, mRNA sequence.

ACCESSION CF328811
VERSION CF328811.1 GI:33605864
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Emaritoidae; Oryzae; Oryza. 1 (bases 1 to 27)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
JOURNAL Contact: Nahm B.H.
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-009"
/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_1lb="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 27;

Best Local Similarity 81.5%; Pred. No. 1.6e+02; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5381 AATTAAAGATTAAAAATACAAAA 5407
DB 27 AAAAAAAAAAATTAATAAAAAAAAA 1

RESULT 131
CF329725/c 27 bp mRNA linear EST 18-AUG-2003
LOCUS NACL-05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL-05-C12, mRNA
sequence.

ACCESSION CF329725 GI:33807665

VERSION CF329725
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-05-C12"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_1lb="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 27;

Best Local Similarity 81.5%; Pred. No. 1.6e+02; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAGATTAAAAATACAAAA 5415
DB 27 AAAAAAAAAAATTAATAAAAAAAAA 1

RESULT 132
CF330557/c 27 bp mRNA linear EST 18-AUG-2003
LOCUS NACL-06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL-06-F04, mRNA
sequence.

ACCESSION CF330557

VERSION CF330557.1 GI:33809352
KEYWORDS EST.

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-06-F04"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_1lb="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 27;

Best Local Similarity 81.5%; Pred. No. 1.6e+02; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAGATTAAAAATACAAAA 5415
DB 27 AAAAAAAAAAATTAATAAAAAAAAA 1

RESULT 133
CF335229/c 27 bp mRNA linear EST 18-AUG-2003

LOCUS JMT--04-N08.b1 ActMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-N08, mRNA sequence.

ACCESSION CF335229 GI:33818810

VERSION CF335229
KEYWORDS EST.

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:33947"
/clone="JMT--04-N08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1ib="AtUMT-overexpressing transgenic rice plasmid
CDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis thaliana Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAATACAAAAAGAAAAA 5415
DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 134
CN545326/C
LOCUS
DEFINITION
EST 17370 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
CN545326
ACCESSION
VERSION
KEYWORDS
ORGANISM
SOURCE
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)

Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

JOURNAL
COMMENT

FEATURES
source

Location/Qualifiers
1..27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL006G12"
/dev_stage="green stage"
/clone_1ib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAATACAAAAAGAAAAA 5415
DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 135
CN545492
LOCUS
DEFINITION
EST 17436 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00GL005G05 3', mRNA sequence.
CN545492.1 GI:46910117

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source

Location/Qualifiers
1..27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL005G05"
/dev_stage="green stage"
/clone_1ib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAATACAAAAAGAAAAA 5415
DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 136
CN545530/C
LOCUS
DEFINITION
EST 17474 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL003B09 3', mRNA sequence.
CN545530
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)

Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne

JOURNAL
COMMENT

Query Match	0.3%;	Score 19;	DB 1;	Length 27;
Best Local Similarity	81.5%;	Pred. No. 1.6e+02;		

REFERENCE
AUTHORS
1 (baves 1 to 27)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barriau, F.,

Couture, C., Dedaldecamp, F., Delort, S., Gillesant, D., Grimples, T.,
 Hamdi, S., Romieu, C. and Terrier, N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)
 Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Université de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33683 Villenave D'Ornon Cedex
France
Tel : 00-33 - (0) 5-57-12-25-50
Fax: 00-33 - (0) 5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seg primer: TV : 00-33 - (0) 5-57-12-25-48

```

FEATURES
  source
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        /organism="Vitis vinifera"
        /mol_type="mRNA"
        /cultivar="Cabernet Sauvignon"
        /db_xref="taxon:29760"
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        /dev_stage="ripening stage"
        /clone_1ib="Ripe Grape Skin Triplex2 library"
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Query Match 0.3%; Score 19; DB 1; length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 5389 AATTAAAAAATACAAAAAGAAAA 5415
   |||||
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 140	LOCUS	DEFINITION	Accession
CN546052/C	CN546052	EST 18004 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL007H09 3', mRNA sequence.	27 bp mRNA linear EST 30-APR-2000

VERSION	CMS46052.1	GI:46910677
KEYWORDS	EST.	
SOURCE	Vitis vinifera	
ORGANISM	Vitis vinifera	

REFERENCE
AUTHORS

Euryarchaea; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal, P., Agassse, A., Ageorges, A., Atanasova, R., Barrieu, F.,

TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL	Unpublished (2002)
COMMENT	Contact: Hamdi S. hamdi@agr.mcgill.ca

UMR 619 - Equipe Biologie de la Vigne
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France

France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7:

```

FEATURES
source
location/Qualifiers
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL007H09"

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/dev_stage="ripening stage"
/clone_lib="ripe Grape Skin Triplex2 library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1
sf1A; Site_2: sf1B; Oriented library"

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Best Local Similarity	81.5%	Pred. No. 1.6e+02		
Matches	22	Conservative	0	Mismatches 5
				Indels 0
				Gaps 0
Qy	5389	AAATTAAAAATACAAAAAGAAAAA	5415	
Db	27	AAAAAAAAAAAAAAAAAAAAAAAAA	1	

RESULT 141				
CN546271/c				
LOCUS	CN546271	27 bp	mRNA	linear
DEFINITION	EST 18223 Green Grape Berry Lambda Triplex2 Library			EST 30-APR-2004
	CDNA clone B5CS1XGB015002 3', mRNA sequence.			Vitis vinifera

ACCESSION	CN546271
VERSION	CN546271.1
KEYWORDS	GI:46910896
SOURCE	EST.
ORGANISM	<i>Vitis vinifera</i>
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS
1 (bases 1 to 27)
Abbal, P., Agasse, A., Ageorges, A., Acanassova, R., Barrieu, F.,
Coute, C., Dedalechamp, F., Delort, S., Gissant, D., Grimplet, J.,
Hamdi, S., Romlet, C. and Terrier, N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)

Université de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-40

FEATURES	
Seq primer: T7.	Email: s.hamdi@orange.fr
Location/Qualifiers	
1..27	

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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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/more_organ="Fruit without seeds; Vector: lambda
Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"

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Matches	22;	Conservative	0;	Mismatches 5;
				Indels 0;
				Gaps 0;

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Oy      5389 AATTAAAAAAAAATACAAAAAAAAAGAAAAA 5415
        || ||||| | ||||| |||||
Db      27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
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RESULT	142	
CNS46337/c		
LOCUS		
DEFINITION	27 bp	mRNA
	EST 18289	Green Grape Berry Lambda Triplex2 Library
	CDNA clone B3CS1XGB01508 3',	Vitis vinifera
	CNS46337	sequence.
ACCESSION		
VERSION		
KEYWORDS		
EST.	GI:46910962	

SOURCE
ORGANISM
Vitis vinifera
Bukayocsa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)

REFERENCE
AUTHORS
Abbal, P., Agase, A., Ageorges, A., Atanaseova, R., Barrieu, F.,
Couture, C., Dedalechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
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1. .27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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/dev_stage="green stage"
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/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"

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Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATCAAAAAGAAAAA 5415
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 143
CN546559/c
LOCUS
DEFINITION
EST 18703 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS58RB008C12 3', mRNA sequence.
CN546559
ACCESSION
VERSION
KEYWORDS
EST.
SOURCE
ORGANISM
Vitis vinifera
Bukayocsa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)

REFERENCE
AUTHORS
Abbal, P., Agase, A., Ageorges, A., Atanaseova, R., Barrieu, F.,
Couture, C., Dedalechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

JOURNAL
COMMENT

FEATURES
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1. .27
/organism="Vitis vinifera"
/mol_type="mRNA"
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/db_xref="taxon:29760"
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/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"

Query Match
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATCAAAAAGAAAAA 5415
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 144
CN546574/c
LOCUS
DEFINITION
EST 18718 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS58RB008E04 3', mRNA sequence.
CN546574
ACCESSION
VERSION
KEYWORDS
EST.
SOURCE
ORGANISM
Vitis vinifera
Bukayocsa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)

REFERENCE
AUTHORS
Abbal, P., Agase, A., Ageorges, A., Atanaseova, R., Barrieu, F.,
Couture, C., Dedalechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
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France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

JOURNAL
COMMENT

FEATURES
source
1. .27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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/dev_stage="ripe stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"

Query Match
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATCAAAAAGAAAAA 5415
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 145

NB9936/c 27 bp mRNA linear EST 02-APR-1996
 LOCUS zB2e12.s1 Soares fetal lung NBH19W Homo sapiens cDNA clone
 DEFINITION IMAGE:302926.3, similar to gb:X59066 ATP SYNTHASE ALPHA CHAIN,
 MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION NB9936
 VERSION NB9936.1 GI:1443263
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 27)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Hollman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevaethick, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watscn.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: RT primer
 High quality sequence stop: 8.
 FEATURES
 source
 1..27
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:1247858"
 /db_xref="taxon:9606"
 /clone="IMAGE:302926"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal lung NBH19W"
 /note="Organ: lung; Vector: pT7R3D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo (dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTT-3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7R3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NBH19W."
 Query Match 0.3%; Score 19; DB 1; Length 27;
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 5389 AATTAAAAAATACAAAAAGAAAAA 5415
 Db 27 AATGCAAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 146
 AZ344642/c 27 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ344642
 DEFINITION 1M0078H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0078H15 R, genomic survey sequence.
 ACCESSION AZ344642
 VERSION AZ344642
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weise, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insect Length: 10000 Std Error: 0.00
 Plate: 0078 row: H column: 15
 Seq primer: CACACGAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.
 FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0078H15"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (9114732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into cells
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 Query Match 0.3%; Score 19; DB 1; Length 27;
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 5389 AATTAAAAAATACAAAAAGAAAAA 5415
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 147
 AZ401672/c 27 bp DNA linear GSS 03-OCT-2000
 LOCUS AZ401672
 DEFINITION 1M0168R04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0168R04 R, genomic survey sequence.
 ACCESSION AZ401672
 VERSION AZ401672
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0168 row: K column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1..27
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0168K04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42uv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAATTAATCAATTAATGAATTA 5415
 DB 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 148
 LOCUS A2434285 27 bp DNA linear GSS 03-OCT-2000
 DEFINITION IM0220B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0220B08 R, genomic survey sequence.
 ACCESSION A2434285
 VERSION A2434285.1 GI:10558298
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0220 row: B column: 08
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.
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 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="UUGC1M0220B08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42uv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;
 Best Local Similarity 81.5%; Pred. No. 1.6e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5398 AATACAAAAAGAAAAATGAAATTA 5424
 DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 149
 LOCUS A2458228 27 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM0262C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0262C12 F, genomic survey sequence.
 ACCESSION A2458228
 VERSION A2458228.1 GI:10616353
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE Niederhausern, A. and Wright, D., Weis, R.
JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0331 row: E column: 14
 Seq primer: CGTTGTAAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES

1. .27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0357B11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5399 ATGCAAAAAGAAAAATGAAATATA 5425
Db 27 AAGAAAAAGAAAAAGAAAAA 1

RESULT 152 27 bp DNA linear GSS 05-OCT-2000
AZ511894/C 1M0357B11P Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0357B11 F, genomic survey sequence.
ACCESSION AZ511894
VERSION AZ511894.1 GI:10693210
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
 Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0357 row: E column: 11
 Seq primer: CGTTGTAAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES

1. .27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0357B11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAATACAAAAAGAAAAA 5415
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 153 27 bp DNA linear GSS 13-DEC-2000
AZ580921/C 1M0369E24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0369E24 F, genomic survey sequence.
ACCESSION AZ580921
VERSION AZ580921.1 GI:11695417
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0365 row: E column: 24
Seq primer: CGTGTGAACACACGCCACGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

SOURCE

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0369E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAAA 5415

DB 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 154
AZ616094/c 27 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0445E17R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0445E17 R, genomic survey sequence.
ACCESSION AZ616094
VERSION AZ616094.1 GI:11738284
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0445 row: E column: 17
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

SOURCE

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0445E17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAAAAA 5415

DB 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 155
AZ623186/c 27 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0460D12R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0460D12 R, genomic survey sequence.
ACCESSION AZ623186
VERSION AZ623186.1 GI:11745376
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: D column: 12
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

1..27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460D12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5389 AATTAAAAAATACAAAAAGAAAAA 5415
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 156
AZ627847/c 27 bp DNA linear GSS.13-DEC-2000
LOCUS AZ627847
DEFINITION 1M0674011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ627847
VERSION AZ627847.1 GI:11750133
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: O column: 11
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

1..27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474O11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5389 AATTAAAAAATACAAAAAGAAAAA 5415
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 157
AZ809295 27 bp DNA linear GSS.20-FEB-2001
LOCUS AZ809295
DEFINITION 2M0073B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ809295
VERSION AZ809295.1 GI:12975450
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: B column: 15
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

1..27
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0073B15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAATAATACAAAAGAAAA 5415
Db 1 AAAAAAAAAAAAAAAAAAAAAA 27

RESULT 158
TA355B06P 27 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 355b06, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL493923
VERSION AL493923.1 GI:11870552
KEYWORDS GSS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 27)
REFERENCE Hall, N., Bowman, S., Lemard, N.J., Doggett, J., Atkin, R.,
AUTHORS Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
TITLE Melville, S.E., Rajandream, M.A. and Barrell, B.G.
JOURNAL Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..27
Location/Qualifiers

/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="J355b06"

Query Match 0.3%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5389 AATTAAATAATACAAAAGAAAA 5415
Db 1 AAAAAAAAAAAAAAAAAAAAAA 27

RESULT 159
A2382013 23 bp DNA linear GSS 02-OCT-2000
LOCUS 1W0138M14R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0138M14 R, genomic survey sequence.
ACCESSION A2382013
VERSION A2382013.1 GI:10495713
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
AUTHORS Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0138 row: M column: 14
Seq primer: CACACAGAAACAGCTATGACC
CLASS: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0138M14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

Query Match 0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATGCAAAAAA 5414
|||||
2 AAAAAAAAAATGCAAAAAA 23

RESULT 160
CD43368 24 bp mRNA linear EST 25-JUN-2004
LOCUS IRB8_E10 IRB8_072 Infected Rat Blood-fed (IRB) An.gam. 30 hr
DEFINITION Abdomen Library Anopheles gambiae cDNA 5', mRNA sequence.
ACCESSION CD743368
VERSION CD743368.1 GI:49247179
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.

REFERENCE 1 (bases 1 to 24)
Dana,A.N., Lobo,N.F., Hillemeier,M.B., and Collins,F.H.
Hematophagy-associated gene expression patterns in adult female
Anopheles gambiae mosquitoes
Unpublished (2003)
JOURNAL Contact: Dana A.N.
Frank H. Collins Laboratory
University of Notre Dame
Center for Tropical Disease Research and Training, Dept. of Biol.
Sci., Notre Dame, IN 46556, USA
Tel: 574 - 631 - 3241
Fax: 574 - 631 - 3996
Email: adana@nd.edu

PCR Primers
FORWARD: ctcgggaagcgcgcattgtgttg
BACKWARD: atagactcactatagggcgaattgc
Seq primer: ctcgggaagcgcgcattgtgttg.
Location/Qualifiers

1. 24
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4Atr"
/db_xref="taxon:7165"
/sex="Female"
/issue_type="Abdomens"
/dev_stage="Female adult 5-7 days post eclosion"
/lab_host="R. coli XL1-Blue"
/clone_lib="Infected Rat Blood-fed (IRB) An.gam. 30 hr
Abdomen Library"
/note="Vector: lamdatrip1x2 (Clontech); Site 1: Sfi IA,
Site 2: Sfi IB; Plasmidum berghei-infected rat blood-fed
adult female An. gambiae mosquitoes were flash frozen
after a 30 hour incubation of adult mosquitoes at 19
degrees Celsius. Total RNA extracted from abdomens

separated from remaining carcass. CDNA inserts >500 bp
cloned directionally into ltripleX2; Sfi IA site is 5'.
Non-normalized and Non-amplified plasmid library. Single
pass sequencing reactions from 5' end."

Query Match 0.3%; Score 18.8; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAAAAATGCAAAAAA 5425
|||||
23 AAAAAAAAAATGCAAAAAA 1

RESULT 161
AZ404078 25 bp DNA linear GSS 03-OCT-2000
LOCUS 1M017207F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION Clone UGCG1M017207 F, genomic survey sequence.
ACCESSION AZ404078
VERSION AZ404078.1 GI:10528091
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)
Dunn,D., Moyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0172 row: J column: 07
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

1. 25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M017207"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5394 AAAAAATACAAAAAGAAAAA 5415
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 162

AZ316353

LOCUS

DEFINITION 26 bp DNA linear GSS 29-FEB-2000
1M0034D09F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0034D09 F, genomic survey sequence.

ACCESSION

AZ316353

VERSION

AZ316353.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: D column: 09
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.

JOURNAL

COMMENT

FEATURES

source

1..26

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGIM0034D09"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.8; DB 1; Length 26;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAAGAAAAA 5414
|||||
Db 4 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 163

AZ813253

LOCUS

DEFINITION 26 bp DNA linear GSS 20-FEB-2001
2M0080M20F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCG2M0080M20 F, genomic survey sequence.

ACCESSION

AZ813253

VERSION

AZ813253.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: M column: 20
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.

JOURNAL

COMMENT

FEATURES

source

1..26

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG2M0080M20"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 18.8; DB 1; Length 26;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1180 AGAGAAAGAGAGAGAGAGAAAT 1201

Db 24 AGAGAGAGAGAGAGAGAGAT 3

RESULT 164

LOCUS CF638767

DEFINITION D06.G05 Filamentous Forced Diploid Ustilago maydis CDNA 3', mRNA

sequence.

CF638767.1 GI:37402758

EST.

Ustilago maydis

Ustilago maydis

Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;

Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

1 (bases 1 to 25)

Nugent, K.G., Choife, K. and Saville, B.J.

Gene Expression during Ustilago maydis Diploid Filamentous Growth:

EST Library Creation and Analyses

Fungal Genet. Biol. 41 (3), 349-360 (2004)

Contact: Barry J. Saville

Saville Lab

University of Toronto

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada

Tel: 905 569 4702

Fax: 905 828 3792

Email: bsaville@utms.utoronto.ca

Seq primer: T7 Reverse (5' GAGTATGACACTCATATAGG 3')

High quality sequence stop: 25.

Location/Qualifiers

1..25

/organism="Ustilago maydis"

/mol_type="mRNA"

/db_xref="FBI12"

/db_xref="taxon:5270"

/cell_type="mycelia"

/dev_stage="Filamentous diploid"

/clone_lib="Filamentous Forced Diploid"

/note="Vector: pSPORT; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

Query Match 0.3%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 1.6e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

5393 AAAAAATACAAAAAGAAAAATG 5417

Db 1 AAAAAAAGAAAAAAGAAAAAAG 25

RESULT 165

LOCUS NS9260

DEFINITION NS9260 25 bp mRNA linear EST 23-FEB-1996

clone IMAGE:289557 3' similar to gp:NT7693 DIAMINE

ACETYLTRANSFERASE (HUMAN); mRNA sequence.

NS9260.1 GI:1203150

EST.

Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 25)

Hillier, L., Clark, N., Dubucq, T., Elliston, K., Hawking, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,

Trevaskis, B., Waterston, R., Williamson, A., Woldmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

This clone is available royalty-free through LML; contact the

IMGS Consortium (info@imgsc.lml.gov) for further information.

Trace considered overall poor quality

Seq primer: m13 -40 forward

High quality sequence stop: 1.

Location/Qualifiers

1..25

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="CDB:3905397"

/db_xref="taxon:9606"

/clone="IMAGE:289557"

/sex="male"

/tissue_type="multiple sclerosis lesions"

/dev_stage="Age 46"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares multiple sclerosis 2NBHSP"

/note="Vector: pT73D (Pharmacia) with a modified

polylinker V-TYPR: phagemid; Site 1: Not I; Site 2: Eco

RI; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'

TGTTACCATCTGAGTGGAGCGCCGATTTTTTTTTTTTTTTT 3'];

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis

lesions from one patient was kindly provided by Dr. Kevin

G. Becker (NINDS/NIH)."

Query Match 0.3%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 1.6e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

5389 AATTAAAAATACAAAAAGAAA 5413

Db 25 AATTAAAAAAGAAAAAAGAAAAA 1

RESULT 166

LOCUS AZ355083

DEFINITION AZ355083 26 bp DNA linear GSS 02-OCT-2000

clone UGCGIM0094D14 R, genomic survey sequence.

AZ355083

VERSION AZ355083.1 GI:10467134

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

Dunn, D., Moyagi, A., Barber, M., Beccorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenan, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 14
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0094D14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 18.6; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5401 ACNAAAAAGAAAAATGAAATGAA 5425
Db 1 AAAAAAAAAAAAAAAAAATRAAAAAA 25

RESULT 167
AZ637459/c 26 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0225B15R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0225B15 R, genomic survey sequence.
ACCESSION AZ637459
VERSION AZ637459.1 GI:10561472
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: B column: 15
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0225B15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 18.6; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAAATG 5417
Db 26 AAAAAAAAAACAAAAAGAAAAAATG 2

RESULT 168
AZ623156 26 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0460U01R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0460U01 R, genomic survey sequence.
ACCESSION AZ623156
VERSION AZ623156.1 GI:11745346
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAGA 1199

DB 21 AGAGAGAGAGAGAGAGAGA 2

RESULT 171
AJ695799/c

LOCUS AJ695799 23 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ695799 Bos taurus cDNA clone KN261-055_007, mRNA sequence.
ACCESSION AJ695799
VERSION AJ695799.1 GI:49429218
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 23)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -mnscore 20 and -mismatch 12 options. Vector: BluescriptII(SK+) R. Site1: EcoRI R. Site2: SmaI 5' Seg Primer T3 Normalised library constructed from bovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.airgenomics.org.
Location/Qualifiers

FEATURES
source

1..23
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-055_007"
/cissue_type="ovary"
/clone_lib="KN261"
/note="Vector: BluescriptII(SK+); Site 1: EcoRI; Site 2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."

Query Match 0.3%; Score 18.2; DB 1; Length 23;

Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415

DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 172

AJ747297

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE Development of a porcine cDNA microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Hopwood PA
Dept. of Preclinical Veterinary Sciences
Royal School for Veterinary Studies
Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM
Sequencing was performed by ARK genomics. This clone is available from ARK-Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS, UK. See www.ark-genomics.org or contact info@arkgenomics.org.

FEATURES
source

1..23
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9623"
/clone="R_1_D05"
/cissue_type="lung"
/cell_type="macrophage"
/clone_lib="reverse - unstimulated minus stimulated macrophage"

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415

DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 173

CP279238/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CP279238 23 bp mRNA linear EST 14-AUG-2003
14ETL--05-H12.gi Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-H12, mRNA sequence.
CP279238
CP279238.1 GI:33656624
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

```
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14EFL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice etiolated leaf plasmid cDNA library
(14EFL)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 174
CP297943/C 23 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--01-B24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-B24, mRNA
sequence.
ACCESSION CP297943
VERSION CP297943.1 GI:33669704
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-B24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAATACAAAAAGAAAAA 5415
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 175
CP310501/C 23 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-C24.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-C24, mRNA sequence.
ACCESSION CP310501
VERSION CP310501.1 GI:33682262
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--05-C24"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABF-responsible
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 176
CP319212/C 23 bp mRNA linear EST 15-AUG-2003
LOCUS HD--09-K06.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-K06, mRNA sequence.
ACCESSION CP319212
VERSION CP319212.1 GI:33690973
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

DEFINITION NACL--05-B19.B1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-B19, mRNA sequence.

ACCESSION CP329694.1 GI:33807601

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)

AUTHORS Song,S.-I., Kim,J.K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.-I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-B19"
/tissue_type="callus"
/dev_stage="Proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR-TOPO; Site 1: ScaRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 TTTAAATAATACAAAGAGAAA 5413
Db 23 TTTAAATAATACAAAGAGAAA 1

RESULT 180

LOCUS CP329694.1 23 bp mRNA linear EST 18-ANG-2003

DEFINITION JMT--04-A14.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CP329694.1 GI:33807601

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.-I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--04-A14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR-TOPO; Site 1: ScaRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis thaliana mature leaf."
methyltransferase overexpression line."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 TTTAAATAATACAAAGAGAAA 5415
Db 1 TTTAAATAATACAAAGAGAAA 23

RESULT 181

LOCUS CN545940 23 bp mRNA linear EST 30-ADR-2004

DEFINITION EST 17885 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL006F03 3', mRNA sequence.

ACCESSION CN545940

VERSION EST.

KEYWORDS Vitis vinifera

SOURCE Vitis vinifera

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 23)

AUTHORS Abbal,P., Agase,A., Ageorges,A., Atanasova,R., Barileu,F., Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

JOURNAL Unpublished (2002)

COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Université de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.

FEATURES
source

1..23
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006F03"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: lambda Triplex2; Site 1: ScaRI; Site 2: SfiIB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 TTTAAATAATACAAAGAGAAA 5415


```

Db      23  ||||| | ||||| |||||
        23  AAAAAAAAAAAAAAAAAAAAA 1

RESULT 182
CN546520/C      23 bp      mRNA      linear      EST 30-APR-2004
LOCUS      EST 18664 Ripe Grape Berry lambda Triplex2 library vltis vinfiera
DEFINITION      CDNA clone B3CC57RB007H08 3', mRNA sequence.
ACCESSION      CN546520
VERSION      CN546520.1 GI:46911145
KEYWORDS      EST.
SOURCE      Vltis vinfiera
ORGANISM      Vltis vinfiera
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; Vitaceae; Vitis.
              1 (bases 1 to 23)
REFERENCE      Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
AUTHORS      Couture, C., Dedaldechamp, F., Delrot, S., Gleysant, D., Grimplet, J.,
              Hamdi, S., Komieu, C. and Terrier, N.
              Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
              or seeds) at Various Developmental Stages
              Unpublished (2002)
              Contact: Hamdi S.
              UMR 619 - Equipe Biologie de la Vigne
              Universite de Bordeaux I, Institut National de la Recherche
              Agronomique
              71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
              France
              Tel: 00-33-(0)5-57-12-25-50
              Fax: 00-33-(0)5-57-12-25-48
              Email: s.hamdi@bordeaux.inra.fr
              Seq primer: T7.
              Location/Qualifiers
                1..23
                /organism="Vltis vinfiera"
                /mol_type="mRNA"
                /cultivar="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clone="B3CC57RB007H08"
                /dev_stage="ripe stage"
                /clone_1db="Ripe Grape Berry lambda Triplex2 library"
                /note="Organ: Fruit without seeds; Vector: Lambda
                Triplex2; Site_1: SflIA; Site_2: SflIB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 23;
Beet Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393  AAAAAAAAAACAAAGAAAAA 5415
Db      23  AAAAAAAAAAAAAAAAAAAAA 1

RESULT 183
CN577495/C      23 bp      mRNA      linear      EST 20-JUN-2004
LOCUS      TVEST077D06 TV30236_PT CDNA Library Trichomonas vaginalis cDNA 5',
DEFINITION      mRNA sequence.
ACCESSION      CN577495
VERSION      CN577495.1 GI:50407891
KEYWORDS      EST.
SOURCE      Trichomonas vaginalis
ORGANISM      Trichomonas vaginalis
              Eukaryota; Parabasalidae; Trichomonada; Trichomonadida;
              Trichomonadidae; Trichomonadinae; Trichomonas.
              1 (bases 1 to 23)
REFERENCE      Zhou, Y., Shu, W. M., Huang, S. C. C., Huang, K. Y. and Tang, P.
AUTHORS      Analysis of Gene Expression Profile in Trichomonas vaginalis by EST
              Sequencing
              Unpublished (2003)
              Contact: Tang, P.
              Location/Qualifiers
                1..23
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="U06C1M0013G08"
                /sex="Male"

JOURNAL COMMENT
Contact: Tang, P.

```

```

Molecular Regulation and Bioinformatics Laboratory, College of
Medicine
Chang Gung University
259 Wenhsa 1st. Road, Kweishan, Taoyuan 333, Taiwan
Tel: +886 3 3283016 EXT5136
Fax: +886 3 3283031
Email: petang@mail.cgu.edu.tw
PCR primers
FORWARD: T7
BACKWARD: T3
Seq primer: T3.
              Location/Qualifiers
                1..23
                /organism="Trichomonas vaginalis"
                /mol_type="mRNA"
                /db_xref="taxon:5722"
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                /dev_stage="Trophozoites at mid-log phase"
                /lab_host="XLI Blue-MR"
                /clone_1db="TV30236_PT CDNA Library"
                /note="Vector: Lambda ZAP-Express (Stratagene); Site_1:
                EcoRI; Site_2: XhoI"

Query Match      0.3%; Score 18.2; DB 1; Length 23;
Beet Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393  AAAAAAAAAACAAAGAAAAA 5415
Db      23  AAAAAAAAAAAAAAAAAAAAA 1

RESULT 184
AZ309219/C      23 bp      DNA      linear      GSS 29-SEP-2000
LOCUS      IM0013608F Mouse 10kb plasmid U06C1M library Mus musculus genomic
DEFINITION      clone U06C1M0013G08 F, genomic survey. sequence.
ACCESSION      AZ309219
VERSION      AZ309219.1 GI:10349986
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 23)
REFERENCE      Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
AUTHORS      Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
              Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
              Niederhausern, A. and Wright, D., Weiss, R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: dunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0013 row: G column: 08
              Seq primer: CGTGTAAACACACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 23.
              Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="U06C1M0013G08"
                /sex="Male"

JOURNAL COMMENT
Contact: Robert B. Weiss

```

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415

Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 185

AZ309851

LOCUS AZ309851 23 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0017112F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0017112 F, genomic survey sequence.

ACCESSION AZ309851
VERSION AZ309851.1 GI:10351256

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

REFERENCE

AUTHORS

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00

Plate: 0017 row: 1 column: 12
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends

High quality sequence stop: 23.
Location/Qualifiers

FEATURES

SOURCE

1. 23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0017112"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 186

AZ312314

LOCUS AZ312314 23 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0028006F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0028006 F, genomic survey sequence.

ACCESSION AZ312314
VERSION AZ312314.1 GI:10356138

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

REFERENCE

AUTHORS

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00

Plate: 0028 row: 0 column: 06
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends

High quality sequence stop: 23.
Location/Qualifiers

FEATURES

SOURCE

1. 23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0028006"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 187
A2313922 23 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0030A02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M030A02 R, genomic survey sequence.
ACCESSION A2313922
VERSION A2313922.1 GI:10359299
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0030 row: A column: 02
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M030A02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 188
A2351354 23 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0089D19P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0089D19 F, genomic survey sequence.
ACCESSION A2351354
VERSION A2351354.1 GI:10430591
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: D column: 19
Seq primer: CGTGTAAACGACGCCAGC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089D19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 189
A2357645 23 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0099C3P Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0099C3 P, genomic survey sequence.

ACCESSION A2357645
VERSION A2357645.1 GI:10471345

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhuesern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: C column: 23
Seq primer: CGTTGTAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source 1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0099C23"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 190
A2419236 23 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0195H07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0195H07 R, genomic survey sequence.

ACCESSION A2419236
VERSION A2419236.1 GI:10543249

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhuesern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0195 row: H column: 07
Seq primer: CACACGGAACACGATGAC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source 1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0195H07"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAA 5415
||||| ||||| ||||| ||||| |||||
Db 23 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 191
A2461220 23 bp DNA linear GSS 04-OCT-2000
LOCUS A2461220
DEFINITION 1M0267005F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0267005 F, genomic survey sequence.
ACCESSION A2461220
VERSION A2461220.1 GI:10619345
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: D column: 05
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source 1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0267005"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAAGAAAAA 5415
||||| ||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 192
A2465327 23 bp DNA linear GSS 04-OCT-2000
LOCUS A2465327/c
DEFINITION 1M02755K12P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M02755K12 F, genomic survey sequence.
ACCESSION A2465327
VERSION A2465327.1 GI:10623452
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: K column: 12
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source 1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0275K12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 193
AZ481702/c 23 bp DNA 1linear GSS 04-OCT-2000
LOCUS
DEFINITION
clone UUGC1M0306B11 F, genomic survey sequence.

ACCESSION
AZ481702.1 GI:10642767

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0306 Row: B Column: 11

Seq primer: CGTGTGAAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. 23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0306B11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 194
AZ588254/c 23 bp DNA 1linear GSS 13-DEC-2000
LOCUS
DEFINITION
clone UUGC1M0396024 F, genomic survey sequence.

ACCESSION
AZ588254.1 GI:11710444

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0306 Row: O Column: 24

Seq primer: CGTGTGAAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. 23

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0396024"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAAAGAAAAA 5415
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 195
LOCUS AZ593540 23 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0405C07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0405C07 F, genomic survey sequence.
ACCESSION AZ593540
VERSION AZ593540.1 GI:11715730
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0405 row: C column: 07
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0405C07"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAAAGAAAAA 5415
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 196
LOCUS AZ610785 23 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0436N07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0436N07 F, genomic survey sequence.
ACCESSION AZ610785
VERSION AZ610785.1 GI:11732975
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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84112, USA
Tel: 801 585 5606
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: N column: 07
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0436N07"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 197
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LOCUS 1M0514E09F Mouse 10kb plasmid UUGCM library Mus musculus genomic
DEFINITION clone UUGCM0514E09 F, genomic survey sequence.
ACCESSION AZ647637
VERSION AZ647637.1 GI:11779301
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Moyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0514 row: B column: 09
Seq primer: CGTGTGAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

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/clone="UUGCM0514E09"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UUGCM library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 198
AZ654903 23 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0529D03R Mouse 10kb plasmid UUGCM library Mus musculus genomic
DEFINITION clone UUGCM0529D03 R, genomic survey sequence.
ACCESSION AZ654903
VERSION AZ654903.1 GI:11792049
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Moyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 03
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

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/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UUGCM library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5415
Db 1 AAAAAAAAAAAAAAAAAA 23

RESULT 199
A278751 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0014008F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0014008 F, genomic survey sequence.
ACCESSION A278751
VERSION A278751.1 GI:12908711
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: 0 column: 08
Seq primer: CGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

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/clone="UUGC2M0014008"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

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Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5415
Db 1 AAAAAAAAAAAAAAAAAA 23

RESULT 200
A2787184 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0033C07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0033C07 F, genomic survey sequence.
ACCESSION A2787184
VERSION A2787184.1 GI:12925692
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: C column: 07
Seq primer: CGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source 1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0033C07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

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Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 201
A2792751 23 bp DNA 1linear GSS 16-FEB-2001
LOCUS A2792751/c
DEFINITION 2M0045K24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045K24 F, genomic survey sequence.

ACCESSION A2792751
VERSION A2792751.1 GI:12937005
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

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JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES
source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0045K24"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

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Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 202
A2859570 23 bp DNA 1linear GSS 21-FEB-2001
LOCUS A2859570
DEFINITION 2M0165B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0165B14 F, genomic survey sequence.

ACCESSION A2859570
VERSION A2859570.1 GI:13054022
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES
source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0165B14"
/sex="Male"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to

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Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5415
|||||
1 AAAAAAAAAAAAAAAAAA 23

RESULT 203

AZ939608 23 bp DNA linear GSS 26-APR-2001
LOCUS 2M0198107R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION Clone UUGC2M0198107 R, genomic survey sequence.

ACCESSION AZ939608
VERSION AZ939608.1 GI:13800390

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 23)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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JOURNAL Unpublished (2000)
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FEATURES
source
1.23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0198107"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnars/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

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Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5415
|||||
1 AAAAAAAAAAAAAAAAAA 23

RESULT 204

BH000534 23 bp DNA linear GSS 27-APR-2001
LOCUS 2M0288B03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION Clone UUGC2M0288B03 R, genomic survey sequence.

ACCESSION BH000534
VERSION BH000534.1 GI:13871760

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 23)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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FEATURES
source
1.23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288B03"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnars/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 205
LOCUS TA151C020
DEFINITION T. brucei sheared genomic DNA clone 151C02, reverse sequence,
genomic survey sequence.

ACCESSION AL473028 GI:11838301
VERSION
KEYWORDS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Bukariyoca; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="151C02"

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 206
LOCUS TA274B03P
DEFINITION T. brucei sheared genomic DNA clone 274B03, forward sequence,
genomic survey sequence.

ACCESSION AL484584 GI:11851281
VERSION
KEYWORDS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Bukariyoca; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274B03"

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 207
LOCUS TA333A10P
DEFINITION T. brucei sheared genomic DNA clone 333A10, forward sequence,
genomic survey sequence.

ACCESSION AL494456 GI:11870913
VERSION
KEYWORDS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Bukariyoca; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..23
Location/Qualifiers

/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="353a10"

Query Match 0.3%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAA 5415
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 208
LOCUS AW247159 24 bp mRNA linear EST 07-JUN-2000
DEFINITION 2819627.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819627 3',
mRNA sequence.

ACCESSION AW247159
VERSION AW247159.1 GI:6590152
KEYWORDS EST.
SOURCE Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 24)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819627.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: DCTP/DRP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnlnl.gov/bhrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 24
contiguous PHRED high quality bases following vector sequence. Very
low Quality Sequence: Trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.

Plate: L16M2 row: B column: 12
High quality sequence stop: 24.

FEATURES
source Location/Qualifiers

1..24

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819627"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match

0.3%; Score 18.2; DB 1; Length 24;

Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAAAAATCAAAATATAA 5425
|||||
Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 209
LOCUS BG670391 24 bp mRNA linear EST 30-APR-2001
DEFINITION DRNBAP06 Rat DRG Library Rattus norvegicus cDNA clone DRNBAP06 5',
mRNA sequence.

ACCESSION BG670391
VERSION BG670391.1 GI:13892490
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
1 (bases 1 to 24)
Xiao H.S., Huang Q.H., Zhang F.X., Bao L., Lu Y.J., Guo C.,
Yang L., Huang W.J., Fu G., Xu S.H., Cheng X.P., Yan Q., Zhu Z.D.,
Zhang X., Chen Z., Han Z.G. and Zhang X.
Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
22056133
12060780
Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-66474870-121
Fax: 86-21-664713446
Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@hgc.sh.cn)

PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3

POLYA=No.

FEATURES
source Location/Qualifiers

1..24

/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNBAP06"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_1ib="Rat DRG Library"

Query Match 0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAA 5415
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 210
LOCUS BX554611 24 bp mRNA linear EST 10-OCT-2003
DEFINITION BX554611 Gloesina morsitans morsitans adult infected gut Gloesina
morsitans morsitans cDNA clone Tse16d06_pic, mRNA sequence.

ACCESSION BX554611

VERSION BX554611.1 GI:33378684
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 24)
 REFERENCE Lehane,M.J., Aksoy,S., Gibson,M., Kethornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J.Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.
 FEATURES
 source
 1..24
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse16d06_plc"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"
 Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 ||||| ||||| ||||| |||||
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 2
 RESULT 211
 CF276855 24 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--02-C19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-C19,
 mRNA sequence.
 ACCESSION CF276855
 VERSION CF276855.1 GI:33654241
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; Oryza.
 1 (bases 1 to 24)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 FEATURES
 source
 1..24
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--02-C19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 23
 RESULT 212
 CF281313 24 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--08-F05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--08-F05,
 mRNA sequence.
 ACCESSION CF281313
 VERSION CF281313.1 GI:33658700
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; Oryza.
 1 (bases 1 to 24)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 FEATURES
 source
 1..24
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--08-F05"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Oy 5393 AAAAAAAAAAGAAAAA 5415
 |||||
 Db 23 AAAAAAAAAAAAAAAAAA 1

RESULT 213
 CF301561 24 bp mRNA linear EST 15-AUG-2003
 LOCUS CF301561/c
 DEFINITION 7LEAF--06-H15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--06-H15, mRNA
 sequence.

ACCESSION
 VERSION CF301561
 KEYWORDS
 SOURCE

ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eubartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 24)

AUTHORS
 TITLE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..24
 location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--06-H15"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO, site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAAGAAAAA 5415
 |||||
 Db 24 AAAAAAAAAAAAAAAAAA 2

RESULT 214
 CF320862 24 bp mRNA linear EST 15-AUG-2003
 LOCUS CF320862/c
 DEFINITION HD--11-O12.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--11-O12, mRNA sequence.

ACCESSION
 VERSION CF320862
 KEYWORDS
 SOURCE

ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eubartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 24)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..24
 location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--11-O12"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2M6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: PCR4-TOPO, site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAAGAAAAA 5415
 |||||
 Db 24 AAAAAAAAAAAAAAAAAA 2

RESULT 215
 CN545249 24 bp mRNA linear EST 30-APR-2004
 LOCUS CN545249/c
 DEFINITION EST 17193 Green Grape Skin Triplex2 library Vitis vinifera cDNA
 clone B3CS00GL004H11 3', mRNA sequence.

ACCESSION
 VERSION CN545249
 KEYWORDS
 SOURCE

ORGANISM
 Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.

REFERENCE
 1 (bases 1 to 24)
 Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,
 Couture, C., Dedaldechamp, F., Delrot, S., Gilsant, D., Grimplet, J.,
 Hamdi, S., Romieu, C. and Terrier, N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)

TITLE
 JOURNAL
 COMMENT
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-46
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: 17.
 location/Qualifiers

FEATURES
 source
 1..24
 location/Qualifiers
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:28760"
 /clone="B3CS00GL004H11"

```

/dev stage="green stage"
/clone_1lb="Green Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
Site1, Site_2: SiteB, Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 216
CN545307/c 24 bp mRNA 1linear EST 30-APR-2004
LOCUS EST 17251 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN545307
VERSION CN545307.1 GI:46909932
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 24)
Abbel, P., Agase, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..24
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006B12"
/dev_stage="green stage"
/clone_1lb="Green Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
Site1, Site_2: SiteB, Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 217
CN545657/c 24 bp mRNA 1linear EST 30-APR-2004
LOCUS EST 17601 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN545657
VERSION CN545657.1 GI:46910282
KEYWORDS EST.

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```

SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 24)
Abbel, P., Agase, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
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Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..24
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL004B09"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
Site1, Site_2: SiteB, Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 218
CN545784/c 24 bp mRNA 1linear EST 30-APR-2004
LOCUS EST 17728 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN545784
VERSION CN545784.1 GI:46910409
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 24)
Abbel, P., Agase, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

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FEATURES

Location/Qualifiers
1..24
/organism="Vitis vinifera"
/mol_type="mRNA"
/culti_var="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL005H06"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiI; Site_2: SfiIB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415
|||||
24 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 219
LOCUS CNA546689 24 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18460 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera cDNA clone B3CS37TB007F12 3', mRNA sequence.

ACCESSION CNA546689

VERSION CNA546689.1 GI:46911314

KEYWORDS EST

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

REFERENCE 1 (bases 1 to 24)
Abbal, F., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplec, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
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Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7,
location/Qualifiers

REFERENCE 1 (bases 1 to 24)
Abbal, F., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplec, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
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Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7,
location/Qualifiers

JOURNAL COMMENT

FEATURES

Location/Qualifiers
1..24
/organism="Vitis vinifera"
/mol_type="mRNA"
/culti_var="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007F12"
/dev_stage="ripening stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiI; Site_2: SfiIB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415
|||||
24 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 220

A2328848 24 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0052M17R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0052M17 R, genomic survey sequence.

ACCESSION A2328848

VERSION A2328848.1 GI:10388979

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Bacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: M column: 17
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
location/Qualifiers

REFERENCE 1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Bacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: M column: 17
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
location/Qualifiers

JOURNAL COMMENT

FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0052M17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAAAAAGAAAAA 5415
|||||
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 221
A2363562

LOCUS AZ363562 24 bp DNA linear GSS 02-OCT-2000
 DEFINITION IM0109G10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0109G10 F, genomic survey sequence.
 ACCESSION AZ363562
 VERSION AZ363562.1 GI:10477262
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 REFERENCES
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhuesern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plates: 0109 row: G column: 10
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0109G10"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 ||||| ||||| ||||| |||||
 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23
 Db

RESULT 222
 AZ386491 24 bp DNA linear GSS 02-OCT-2000
 LOCUS

DEFINITION IM0145D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0145D02 R, genomic survey sequence.
 ACCESSION AZ386491
 VERSION AZ386491.1 GI:10500191
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 REFERENCES
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhuesern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plates: 0145 row: D column: 02
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0145D02"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 ||||| ||||| ||||| |||||
 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23
 Db

RESULT 223
 AZ390642 24 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION IM0152H07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

accession clone UGCG1M0152H07 F, genomic survey sequence.
 version AZ390642
 key words AZ390642.1 GI:10505685
 source GSS.
 organism Mus musculus (house mouse)
 reference Mus musculus
 authors Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
 title Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 journal Mouse whole genome scaffolding with paired end reads from 10kb
 comment Unpublished (2000)
 contact: Robert B. Weis
 university of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 tel: 801 585 5606
 fax: 801 585 7177
 email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0152 row: H column: 07
 seq primer: CGTGTGTAACGACGCGCAGT
 class: plasmid ends
 high quality sequence stop: 24.
 features location/Qualifiers
 source 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0152H07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 224
 AZ438069
 LOCUS AZ438069 24 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0228A10F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 accession clone UGCG1M0228A10 F, genomic survey sequence.

accession AZ438069
 version AZ438069.1 GI:10562178
 key words GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 reference Mus musculus
 authors Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
 title Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 journal Mouse whole genome scaffolding with paired end reads from 10kb
 comment Unpublished (2000)
 contact: Robert B. Weis
 university of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 tel: 801 585 5606
 fax: 801 585 7177
 email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0228 row: A column: 10
 seq primer: CGTGTGTAACGACGCGCAGT
 class: plasmid ends
 high quality sequence stop: 24.
 features location/Qualifiers
 source 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0228A10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5394 AAAAAAAAAAAGAAAAAAT 5416
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAT 23

RESULT 225
 AZ458112
 LOCUS AZ458112/2 24 bp DNA linear GSS 04-OCT-2000
 DEFINITION 1M0261R24R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 accession clone UGCG1M0261R24 R, genomic survey sequence.

VERSION AZ458112.1 GI:10616237
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn,D., Hoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Iselm,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0261 row: E column: 24
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0261R24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAAAAAATGAAATATAA 5425
 DB 23 AAAAAAAAAAATATAAAAAA 1

RESULT 226
 AZ459280/c 24 bp DNA linear GSS 04-OCT-2000
 LOCUS IM0454823F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 DEFINITION Clone UGCG1M0264A05 F, genomic survey sequence.
 ACCESSION AZ459280
 VERSION AZ459280.1 GI:10617405

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn,D., Hoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Iselm,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0264 row: A column: 05
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0264A05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAAAAA 5415
 DB 24 AAAAAAAAAAATATAAAAAA 2

RESULT 227
 AZ621257/c 24 bp DNA linear GSS 13-DEC-2000
 LOCUS IM0454823F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 DEFINITION Clone UGCG1M0454823 F, genomic survey sequence.
 ACCESSION AZ621257
 VERSION AZ621257.1 GI:11743447

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: B column: 23
Seq primer: CGTCTGAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0454E23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5403 AAAAAAAAAAATGAAATTA 5425
|||||
Db 24 AAAAAAAAAAATGAAATTA 2

RESULT 228
AZ644621/c 24 bp DNA linear GSS 14-DEC-2000
LOCUS
DEFINITION 1M0508F12R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0508F12 R, genomic survey sequence.
ACCESSION AZ644621
VERSION AZ644621.1 GI:11773331
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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JOURNAL Unpublished (2000)
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University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0508 row: F column: 12
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0508F12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAAA 5415
|||||
Db 24 AAAAAAAAAAAGAAAAA 2

RESULT 229
AZ786257 24 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M0031H1R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0031H1 R, genomic survey sequence.
ACCESSION AZ786257
VERSION AZ786257.1 GI:12923835
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: H column: 11
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0031H11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[4732114|9b|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 |||||
 DB 2 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 230
 LOCUS AZ834990 24 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0129A05P Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG2M0129A05 F, genomic survey sequence.
 ACCESSION AZ834990
 VERSION AZ834990.1 GI:13004898
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0129 row: A column: 05
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0129A05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[4732114|9b|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.7e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 |||||
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 231
 LOCUS AZ970038 24 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0243J02P Mouse 10kb plasmid UUCG2M library Mus musculus genomic clone UUCG2M0243J02 F, genomic survey sequence.
 ACCESSION AZ970038
 VERSION AZ970038.1 GI:13841265
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0243 row: J column: 02
Seq primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0243J02"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 5393 AAAAAAAAAATCAAAAAAGAAAAA 5415
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 232
AZ984490 24 bp DNA linear GSS 27-APR-2001
LOCUS 2M0266H05F Mouse 10kb plasmid UUCG2M library Mus musculus genomic
DEFINITION clone UUCG2M0266H05 F, genomic survey sequence.
ACCESSION AZ984490
VERSION AZ984490.1 GI:13855717
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0266 row: H column: 05
Seq primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0266H05"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 5393 AAAAAAAAAATCAAAAAAGAAAAA 5415
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 233
AZ993423 24 bp DNA linear GSS 27-APR-2001
LOCUS 2M0278019F Mouse 10kb plasmid UUCG2M library Mus musculus genomic
DEFINITION clone UUCG2M0278019 F, genomic survey sequence.
ACCESSION AZ993423
VERSION AZ993423.1 GI:13864650
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)

JOURNAL
COMMENT
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0278 row: 0 column: 19
Seq primer: CGTTGTAAACGACGCCAGCT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
source

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0278019"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: pMD42mv. Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 18.2; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy
5393 AAAAAAAAAACAAAAAAGAAAAA 5415
|||||
24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 234
TA169D12P/C
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 169d12, forward sequence,
genomic survey sequence.
ACCESSION
AL478922
VERSION
AL478922.1 GI:11840452
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 24)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

TITLE
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submissions
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhle@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nhle@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source

1. 24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRBU927"
/db_xref="taxon:5691"
/clone="169d12"

Query Match
Best Local Similarity 0.3%; Score 18.2; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy
5393 AAAAAAAAAACAAAAAAGAAAAA 5415
|||||
24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 235
TA27B08Q
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 27b08, reverse sequence,
genomic survey sequence.
ACCESSION
AL453584
VERSION
AL453584.1 GI:11850982
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 24)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhle@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nhle@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source

1. 24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRBU927"

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/db_xref="taxon:5691"
/clone="37D08"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAATACAAAAAGAAAAA 5415
      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 236
TA354C06P      24 bp      DNA      linear      GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 354c06, forward sequence.
DEFINITION     genomic survey sequence.
ACCESSION     AL494439.1 GI:11870896
VERSION       GSS.
KEYWORDS
SOURCE        Trypanosoma brucei
ORGANISM      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS      1 (bases 1 to 24)
              Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
              Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
              Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE         Direct Submission
JOURNAL       Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT       Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + 1 method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.
              Location/Qualifiers
                source          1..24
                               /organism="Trypanosoma brucei"
                               /mol_type="genomic DNA"
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Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAATACAAAAAGAAAAA 5415
      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 237
TA371P11P      24 bp      DNA      linear      GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 371f11, forward sequence.
DEFINITION     genomic survey sequence.
ACCESSION     AL495622
VERSION       GI:11871906
KEYWORDS      GSS.
SOURCE        Trypanosoma brucei
ORGANISM      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

```

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Trypanosoma.
1 (bases 1 to 24)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE         Direct Submission
JOURNAL       Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT       Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + 1 method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.
              Location/Qualifiers
                source          1..24
                               /organism="Trypanosoma brucei"
                               /mol_type="genomic DNA"
                               /strain="TREU927"
                               /db_xref="taxon:5691"
                               /clone="371f11"

Query Match      0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAATACAAAAAGAAAAA 5415
      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 238
TA95B08P      24 bp      DNA      linear      GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 95b08, forward sequence.
DEFINITION     genomic survey sequence.
ACCESSION     AL459003
VERSION       GI:11861374
KEYWORDS      GSS.
SOURCE        Trypanosoma brucei
ORGANISM      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS      1 (bases 1 to 24)
              Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
              Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
              Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE         Direct Submission
JOURNAL       Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT       Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + 1 method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.
              Location/Qualifiers

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source
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="95D08"

Query Match 0.3%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY 5393 AAAAAAAAAATGACAAAAGAAAAA 5415
||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 239
AU265663 25 bp mRNA linear EST 26-APR-2004
LOCUS AU265663/C
DEFINITION AU265663 VS Dictyostellium discoideum cDNA clone VSR713 5', mRNA
sequence.
ACCESSION AU265663.1 GI:20524461
VERSION AU265663.1
KEYWORDS EST.
SOURCE Dictyostellium discoideum
ORGANISM Dictyostellium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
1 (bases 1 to 25)
Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
Maeda,M., Williams,D.G., Takeuchi,I. and Tanaka,Y.
Analyses of cDNAs from growth and slug stages of Dictyostellium
discoideum
Nucleic Acids Res. 32 (5), 1647-1653 (2004)

JOURNAL Contact: Hideko Urushihara
COMMENT Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
1..25
/organism="Dictyostellium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSR713"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

FEATURES
source
1..25
/organism="Dictyostellium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSR713"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0,

QY 5403 AAAAAAAAAATGAAATTAATA 5425
||||| ||||| ||||| |||||
Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 240
CF291048 25 bp mRNA linear EST 14-AUG-2003
LOCUS CF291048/C
DEFINITION CF291048 -01-P05.b1 Rice root plasmid cDNA library (14RCOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14RCOT--01-P05, mRNA
sequence.
ACCESSION CF291048.1 GI:33660081
VERSION CF291048.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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/clone.lib="Rice root plasmid cDNA library (1400T)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 242
CF299288
LOCUS 7LEAF--03-E01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) CDNA clone 7LEAF--03-E01, mRNA
sequence.

ACCESSION CF299288.1 GI:33671049
VERSION CF299288
KEYWORDS EST
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source location/Qualifiers

1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-E01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone.lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 243
CF300333
LOCUS 7LEAF--04-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) CDNA clone 7LEAF--04-L02, mRNA
sequence.

ACCESSION CF300333
VERSION CF300333.1 GI:33672094
KEYWORDS EST.

SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers

1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="7LEAF--04-L02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone.lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 244
CF301712
LOCUS 7LEAF--06-K21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) CDNA clone 7LEAF--06-K21, mRNA
sequence.

ACCESSION CF301712.1 GI:33673473
VERSION CF301712
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers

1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

/clone="7LEAF--06-K21"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415
Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 245
CF316323/c
LOCUS HD--05-H05.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION 25 bp mRNA linear EST 15-AUG-2003
HD--05-H05, mRNA sequence.
CF316323
CF316323
ACCESSION GI:3368084
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 25)
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 246
CF317714/c

LOCUS CF317714 25 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--07-103.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-103, mRNA sequence.
CF317714
CF317714
ACCESSION GI:33689475
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 25)
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD--07-103"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 247
CF319073/c
LOCUS HD--09-H05.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H05, mRNA sequence.
CF319073
CF319073
ACCESSION GI:33690834
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 25)
Klm,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..25

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="NACL--06-K11"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_1ib="OshDAC1-overexpressing transgenic rice plasmid"

CDNA library (HD) "

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was"

treated with ABA(20um) for 1hr. Oligo-capped mRNA was"

reverse transcribed and then used for PCR. mRNA was"

derived from rice Histone Deacetylase overexpression"

line."

Query Match 0.3%; Score 18.2; DB 1; Length 25;

Best Local Similarity 87.0%; Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 248

CF330786/c

LOCUS NACL--06-K11.b1 Rice callus plasmid CDNA library (NACL) Oryza

DEFINITION sativa (japonica cultivar-group) CDNA clone NACL--06-K11, mRNA

sequence.

ACCESSION CF330786.1 GI:33809794

VERSION CF330786

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 25)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of BioScience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..25

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="NACL--06-K11"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_1ib="Rice callus plasmid CDNA library (NACL) "

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped"

with oligoribonucleotides and then used as templates for"

RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 25;

Best Local Similarity 87.0%; Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 249

CN545505/c

LOCUS EST 17449 Green Grape Skin Triplex2 library Vitis vinifera CDNA

DEFINITION clone B3CS00RL005H06 3', mRNA sequence.

ACCESSION CN545505

VERSION CN545505.1 GI:46910130

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; Vitaceae; Vitis.

1 (bases 1 to 25)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: 17.

Location/Qualifiers

1..25

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00GL005H06"

/dev_stage="green stage"

/clone_1ib="Green Grape Skin Triplex2 library"

/note="Organ: Fruit skin; Vector: lambda Triplex2; Site_1:

SfilA; Site_2: SfilB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 25;

Best Local Similarity 87.0%; Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 250

CN546041/c

LOCUS EST 17993 Ripe Grape Skin Triplex2 library Vitis vinifera CDNA

DEFINITION clone B3CS00RL007G10 3', mRNA sequence.

ACCESSION CN546041

VERSION CN546041.1 GI:46910666

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; Vitaceae; Vitis.

1 (bases 1 to 25)

REFERENCE

AUTHORS Abbal, P., Agase, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedalechamp, F., Delrot, S., Glissant, D., Grimpel, J.,
Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
FEATURES
source
1. .25
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL007G10"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAAAAA 5415
|||||
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 251
LOCUS CNS46397 25 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18350 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS1XGB016E10 3', mRNA sequence.
CNS46397
ACCESSION CNS46397.1 GI:46911022
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Vitis vinifera
Vitis vinifera
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 25)
/db_xref="taxon:29760"
/clone="B3CS7RB007D09"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

REFERENCE
AUTHORS Abbal, P., Agase, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedalechamp, F., Delrot, S., Glissant, D., Grimpel, J.,
Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
FEATURES
source
1. .25
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS7RB007D09"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

FEATURES
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS7RB007D09"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

/clone="B3CS1XGB016E10"
/dev_stage="green stage"
/clone_1lb="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAAAAA 5415
|||||
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 252
LOCUS CNS46477 25 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18621 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS57RB007D09 3', mRNA sequence.
CNS46477
ACCESSION CNS46477.1 GI:46911022
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Vitis vinifera
Vitis vinifera
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; Vitaceae; Vitis.
1 (bases 1 to 25)
/db_xref="taxon:29760"
/clone="B3CS57RB007D09"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

REFERENCE
AUTHORS Abbal, P., Agase, A., Ageorges, A., Atanaseva, R., Barrieu, F.,
Couture, C., Dedalechamp, F., Delrot, S., Glissant, D., Grimpel, J.,
Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
FEATURES
source
1. .25
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007D09"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

FEATURES
source
1. .25
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007D09"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 25)

REFERENCE
AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanaseova, R., Barlieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Gleysant, D., Grimplet, J.,
Hamdi, S., Romeu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
CONTACT: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.
Location/Qualifiers
1..25
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3C38TB008B03"
/dev_stage="veraison stage"
/clone_1ib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: Sflta; Site_2: Sfltb; Oriented library"

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATGCACAAAAGAAAAA 5415
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 254
N33150 25 bp mRNA linear EST 10-JAN-1996
LOCUS N33150
DEFINITION YY06G01.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone
IMAGE:270480 3' similar to gb:U29805 N-ACETYLACTOSAMINE SYNTHASE
(HUMAN);, mRNA sequence.
N33150
ACCESSION N33150
VERSION N33150.1 GI:1153549
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 25)

REFERENCE
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucada, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,
Trevaaskis, B., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1

Source: IMAGE Consortium, LML.
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.
Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3880122"
/db_xref="taxon:9606"
/clone="IMAGE:270480"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_1ib="Soares melanocyte 2NbhM"
/note="Vector: pRTT3 (pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCCGACGATTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRTT3 vector
(pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATGCACAAAAGAAAAA 5415
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 255
A2344725 25 bp DNA linear GSS 29-SEP-2000
LOCUS A2344725
DEFINITION 1M0078124R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0078124 R, genomic survey sequence.
A2344725
ACCESSION A2344725
VERSION A2344725.1 GI:10423962
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: 1 column: 24
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"

/mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0078124"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 256
 AZ350777 25 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0088A04R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 DEFINITION clone UUCG1M0088A04 R, genomic survey sequence.

ACCESSION AZ350777
 VERSION AZ350777.1 GI:10430014
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES
 source
 1.25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0088A04"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 257
 AZ389458 25 bp DNA linear GSS 02-OCT-2000
 LOCUS 1M0150B06F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 DEFINITION clone UUCG1M0150B06 F, genomic survey sequence.

ACCESSION AZ389458
 VERSION AZ389458.1 GI:10503166
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES
 source
 1.25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
 source
 1.25
 /organism="Mus musculus"
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 /strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0150B06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_11b="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAAAAA 5415
 ||||| ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 258
 AZ609234/c 25 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0433119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0433119 R, genomic survey sequence.
 ACCESSION AZ609234
 VERSION AZ609234.1 GI:11731424
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0433 row: H column: 19
 Seq primer: CACACAGAAACAGCTATAC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES
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 /db_xref="taxon:10090"

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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_11b="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAAAAA 5415
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 Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 259
 AZ623157/c 25 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0460L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0460L02 R, genomic survey sequence.
 ACCESSION AZ623157
 VERSION AZ623157.1 GI:11745347
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0460 row: L column: 02
 Seq primer: CACACAGAAACAGCTATAC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES
 source

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0460L02"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
DB 25 AAAAAAAAAAAAAAAAAAAAAA 3

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RESULT 260
LOCUS AZ788646 25 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0035L19R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCG2M0035L19 R, genomic survey sequence.
ACCESSION AZ788646
VERSION AZ788646.1 GI:12928656
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0035 row: L column: 19
Seq primer: CACACAGGAAACGCTATACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. 25
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0035L19"
/sex="Male"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
DB 25 AAAAAAAAAAAAAAAAAAAAAA 3

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RESULT 261
LOCUS AZ832800 25 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0113M21F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCG2M0113M21 F, genomic survey sequence.
ACCESSION AZ832800
VERSION AZ832800.1 GI:13002708
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0113 row: M column: 21
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. 25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0113M21"
/sex="Male"

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FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UGCG2M0035L19"
/sex="Male"

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FEATURES
source
1. 25
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UGCG2M0113M21"
/sex="Male"

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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415
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Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 262
AZ949287 25 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0212008R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0212008 R, genomic survey sequence.
ACCESSION AZ949287
VERSION AZ949287.1 GI:13820514
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: O column: 08
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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/clone="UUGC2M0212008"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAAA 5415
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 263
AZ980407 25 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0257M19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0257M19 F, genomic survey sequence.
ACCESSION AZ980407
VERSION AZ980407.1 GI:13851634
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0257 row: M column: 19
Seq primer: CGTGTAAACAGCAGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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/db_xref="taxon:10090"
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/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"

FEATURES

source

musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 264
LOCUS TA154D03P/c 25 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 154d03, forward sequence,
genomic survey sequence.
ACCESSION AL472971
VERSION AL472971.1 GI:11838244
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 25)
AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M. A. and Barrell, B. G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J. C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1..25
/organism="Trypanosoma brucei"
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/strain="TREU927"
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/clone="154d03"

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5394 AAAAAAAAAACAAAAAGAAAAAT 5416
|||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAT 3

RESULT 265
LOCUS TA324B10P/c 25 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 324e10, forward sequence,
genomic survey sequence.
ACCESSION AL493396
VERSION AL493396.1 GI:11867761
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 25)
AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M. A. and Barrell, B. G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J. C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="324e10"

Query Match 0.3%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
Db 25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 266
LOCUS AJ659204 26 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ659204 KN277 Sus scrofa cDNA clone C0005215_B14, mRNA sequence.
ACCESSION AJ659204
VERSION AJ659204.1 GI:4934335
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (bases 1 to 26)
AUTHORS Anderson, S. I., Finlayson, H. A. and Archibald, A. L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics

Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -tnscore 20 and -mismatch 12 options. Vector: BluescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5'. Seq Primer M13F Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arts.genomics.org.

FEATURES
source
location/Qualifiers

1..26
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005215.B14"
/tissue_type="embryo"
/clone_1fb="KM277"
/note="Vector: pBluescriptII(SK+), Site_1: EcoRI, Site_2: NotI, Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 267
LOCUS AW327613/c 26 bp mRNA linear EST 28-JUN-2000
DEFINITION dq01b09.y1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846536 3', mRNA sequence.
ACCESSION AW327613
VERSION AW327613.1 GI:6798108
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 26)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Edge Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Plate: LHC80028 row: C column: 17
Seq primer: M13RP reverse primer (ABT).
location/Qualifiers

FEATURES
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1..26
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2846536"
/tissue_type="T cell leukemia"
/cell_line="MGC2"
/clone_1fb="NIH_MGC_2"
/note="Organ: Blood; Vector: pOTB7a; Library prepared by Edge Biosystems."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 268
LOCUS BM658913/c 26 bp mRNA linear EST 27-FEB-2002
DEFINITION LOC602768282.R1 CSEQFXL36 fetal brain Sus scrofa cDNA, mRNA sequence.

ACCESSION BM658913
VERSION BM658913.1 GI:18959184
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 26)
NotI; Site 2: EcoRI, sequence 5' of the insert
(5'-NNN...NNNinsert)
GCCAATGACACTCCACCGCGGCGCGGCTGAG. sequence 3' of the insert (AAGATTGCAATACAGCTTATCATCTGACTGAG).
non-normalized library, sequenced 3' with M13R primer.

CONTACT: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.

FEATURES
source
location/Qualifiers

1..26
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/dev_stage="fetal"
/clone_1fb="CSEQFXL36 fetal brain"
/note="Organ: brain; Vector: pBluescript SK+; Site_1: NotI; Site 2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GCCAATGACACTCCACCGCGGCGCGGCTGAG. sequence 3' of the insert (AAGATTGCAATACAGCTTATCATCTGACTGAG).
non-normalized library, sequenced 3' with M13R primer."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415

Db 24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 269
LOCUS BX563414/c 26 bp mRNA linear EST 10-OCT-2003
DEFINITION BX563414 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse66e05_p1c, mRNA sequence.

ACCESSION BX563414
VERSION BX563414.1 GI:33430654
KEYWORDS EST.
ORGANISM Glossina morsitans morsitans
SOURCE Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriaman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW

All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
 source Location/Qualifiers

1..26
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="T866e05_plc"
 /issue_type="adult infected gut"
 /clone_11b="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 18.2; DB 1; Length 26;
 Best Local Similarity 87.0%; Pred. No. 1.9e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 Db 23 AAAAAAAAAACAAAAAGAAAAA 1

RESULT 270
 CF278359/c 26 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--04-D22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-D22,
 mRNA sequence.

ACCESSION CF278359
 VERSION CF278359.1 GI:33655745
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriarctidoideae; Oryzaceae; Oryza.
 1 (bases 1 to 26)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1..26
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--04-D22"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"

/clone_11b="Rice etiolated leaf plasmid cDNA library (14ETL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
 Best Local Similarity 87.0%; Pred. No. 1.9e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 Db 26 AAAAAAAAAACAAAAAGAAAAA 4

RESULT 271
 CF282426 26 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--09-P01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-P01,
 mRNA sequence.

ACCESSION CF282426
 VERSION CF282426.1 GI:33659813
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriarctidoideae; Oryzaceae; Oryza.
 1 (bases 1 to 26)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1..26
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--09-P01"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_11b="Rice etiolated leaf plasmid cDNA library (14ETL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
 Best Local Similarity 87.0%; Pred. No. 1.9e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
 Db 1 AAAAAAAAAACAAAAAGAAAAA 23

RESULT 272
 CF296851/c 26 bp mRNA linear EST 14-AUG-2003
 LOCUS 30DGS--07-G13.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 30DGS--07-G13, mRNA
 sequence.
 ACCESSION CF296851

```

VERSION      CF296851.1 GI:33665884
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euphorbiaceae; Oryzae; Oryza.
REFERENCE    1 (bases 1 to 26)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
                1..26
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
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                /db_xref="taxon:39947"
                /clone="30DS--07-G13"
                /issue_type="leaf"
                /dev_stage="30 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library I (30DS)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAAA 5415
        ||||| ||||| ||||| |||||
        26 AAAAAAAAAAAAAAAAAAAAAA 4

Db

RESULT 273
CF297087      26 bp mRNA linear EST 14-AUG-2003
LOCUS         30DS--07-L18.b1 Rice leaf plasmid cDNA library I (30DS) Oryza
DEFINITION    sativa (japonica cultivar-group) cDNA clone 30DS--07-L18, mRNA
              sequence.
ACCESSION     CF297087
VERSION       CF297087.1 GI:33666120
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euphorbiaceae; Oryzae; Oryza.
              1 (bases 1 to 26)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
                1..26
                /organism="Oryza sativa (japonica cultivar-group)"
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                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="30DS--07-G13"
                /issue_type="leaf"
                /dev_stage="30 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library I (30DS)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

FEATURES
source

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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DS--07-L18"
/issue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAAA 5415
        ||||| ||||| ||||| |||||
        26 AAAAAAAAAAAAAAAAAAAAAA 4

Db

RESULT 274
CF299701      26 bp mRNA linear EST 15-AUG-2003
LOCUS         7LEAF--03-N03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION    sativa (japonica cultivar-group) cDNA clone 7LEAF--03-N03, mRNA
              sequence.
ACCESSION     CF299701
VERSION       CF299701.1 GI:33671462
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euphorbiaceae; Oryzae; Oryza.
              1 (bases 1 to 26)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
                1..26
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="7LEAF--03-N03"
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                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

FEATURES
source

RESULT 275
CF302874      26 bp mRNA linear EST 15-AUG-2003
LOCUS         CF302874/c

```

DEFINITION 7LEAF--08-M19.g1 Rice leaf plasmid cDNA library II (7LEAF) *Oryza sativa* (japonica cultivar-group) cDNA clone 7LEAF--08-M19, mRNA sequence.

ACCESSION CF302874

VERSION CF302874.1 GI:33674635

KEYWORDS EST.

SOURCE *Oryza sativa* (japonica cultivar-group)

ORGANISM *Oryza sativa* (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; *Oryza*.

REFERENCE 1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT Contact: Nahm, B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1..26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415
|||||
26 AAAAAAAAAAAAAAAAAAAAAA 4

Db

RESULT 276
CF311369 26 bp mRNA linear EST 15-AUG-2003
ABF--06-J01.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) *Oryza sativa* (japonica cultivar-group) cDNA clone

DEFINITION ABF--06-J01, mRNA sequence.

ACCESSION CF311369

VERSION CF311369.1 GI:33683130

KEYWORDS EST.

SOURCE *Oryza sativa* (japonica cultivar-group)

ORGANISM *Oryza sativa* (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; *Oryza*.

REFERENCE 1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT Contact: Nahm, B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1..26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_1lb="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415
|||||
26 AAAAAAAAAAAAAAAAAAAAAA 4

Db

RESULT 277
CF311439 26 bp mRNA linear EST 18-AUG-2003
NACU--07-J02.b1 Rice callus plasmid cDNA library (NACU) *Oryza sativa* (japonica cultivar-group) cDNA clone NACU--07-J02, mRNA sequence.

ACCESSION CF311439

VERSION CF311439.1 GI:33811097

KEYWORDS EST.

SOURCE *Oryza sativa* (japonica cultivar-group)

ORGANISM *Oryza sativa* (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzaceae; *Oryza*.

REFERENCE 1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE Unpublished (2003)

JOURNAL

COMMENT Contact: Nahm, B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1..26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_1lb="Rice callus plasmid cDNA library (NACU)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
Db	26	AAAAAAAAAAAAAAAAAAAAA 4											
RESULT 278	CF337311/c												
LOCUS	CF337311/c												
DEFINITION	UMT--07-106.G1 AlUMT-overexpressing transgenic rice plasmid cDNA library (UMT Oryza sativa (japonica cultivar-group) cDNA clone UMT--07-106, mRNA sequence.												
ACCESSION	CF337311												
VERSION	CF337311.1												
KEYWORDS	EST.												
SOURCE	Oryza sativa (japonica cultivar-group)												
ORGANISM	Oryza sativa (japonica cultivar-group)												
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Echaritoidae; Oryzaceae; Oryza.												
AUTHORS	1 (bases 1 to 26)												
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.												
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs												
COMMENT	Unpublished (2003)												
CONTACT	Contact: Nahm B.H.												
GENOMICS	Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Yonsei University												
LOCATION	Yongin, Kyonggi, Korea												
TEL	Tel: 82 31 330 6193												
FAX	Fax: 82 31 321 6355												
EMAIL	Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.												
LOCATION/QUALIFIERS	Location/Qualifiers												
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/clone="UMT--07-106"	/clone="UMT--07-106"												
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/dev_stage="14 days after germination"	/dev_stage="14 days after germination"												
/lab_host="E.coli DH10B"	/lab_host="E.coli DH10B"												
/clone_lib="AlUMT-overexpressing transgenic rice plasmid cDNA library (UMT)"	/clone_lib="AlUMT-overexpressing transgenic rice plasmid cDNA library (UMT)"												
/note="Vector: pCR4-TOP0; Site 1: EcoRI, Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis jasmonic acid Carboxyl methyltransferase overexpression line."	/note="Vector: pCR4-TOP0; Site 1: EcoRI, Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis jasmonic acid Carboxyl methyltransferase overexpression line."												
Query Match	0.3%; Score 18.2; DB 1; Length 26;												
Best Local Similarity	87.0%; Pred. NO.1.9e+02;												
Matches	20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;												
Oy	5393 AAAAAAAAAAGGAAAAA 5415												
Db	24 AAAAAAAAAAGGAAAAA 2												
RESULT 279	CNS45213/c												
LOCUS	CNS45213/c												
DEFINITION	EST 17157 Green Grape Skin Triplex2 library Vitis vinifera cDNA clone B3CS00G1004E11.3, mRNA sequence.												

JOURNAL	TITLE
COMMENT	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages Unpublished (2002)
CONTACT	Contact: Hamdi S. UMR 619 - Equipe Biologie de la Vigne Universite de Bordeaux I, Institut National de la Recherche Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France Tel.: 00-33-(0)5-57-12-25-50 Fax: 00-33-(0)5-57-12-25-48 Email: s.hamdi@bordeaux.inra.fr Seq primer: T7.
SOURCE	location/Qualifiers 1..26 /organism="Vitis vinifera" /mol_type="mRNA" /cultivar="Cabernet Sauvignon" /db_xref="taxon:29760" /clone="B3CS00GL004E11" /dev_stage="green stage" /clone_1lb="Green Grape Skin Triplex2 Library" /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1 SfiIA; Site_2: SfiIB; Oriented library"
Query Match	0.3%; Score 18.2; DB 1; Length 26; Best Local Similarity 87.0%; Pred.No.1.9e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
Oy	5393 AAAAAAAAAACAAAAAGAAAAA 5415 Db 26 AAAAAAAAAAAAAAAAAAAAAA 4
RESULT 280	CNS45225 26 bp mRNA linear EST 30-APR-2004
CNS45225/c	LOCUS
DEFINITION	EST 17169 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION	CNS45225
VERSION	CNS45225.1 GI:46909680
KEYWORDS	EST.
SOURCE	Vitis vinifera
ORGANISM	Vitis vinifera
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophytes, Magnoliophyta; eudicotyledons, core eudicots; rosids; Vitaceae; Vitis.	
REFERENCE	1 (bases 1 to 26) Abbal,P., Agasse,A., Ageorges,A., Aranasova,R., Barrieu,F., Conture,C., Dedaldehand,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N. Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages Unpublished (2002) Contact: Hamdi S. UMR 619 - Equipe Biologie de la Vigne Universite de Bordeaux I, Institut National de la Recherche Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France Tel.: 00-33-(0)5-57-12-25-50 Fax: 00-33-(0)5-57-12-25-48 Email: s.hamdi@bordeaux.inra.fr Seq primer: T7.
TITLE	location/Qualifiers
JOURNAL	1..26
COMMENT	/organism="Vitis vinifera" /mol_type="mRNA" /cultivar="Cabernet Sauvignon" /db_xref="taxon:29760" /clone="B3CS00GL004F11" /dev_stage="green stage" /clone_1lb="Green Grape Skin Triplex2 Library"
FEATURES	
source	

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/Note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB, Oriented library"
Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAAAGAAAAA 5415
      ||||| ||||| ||||| |||||
      26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 281
LOCUS      CN545546
DEFINITION EST 17490 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION  CN545546
VERSION     CN545546
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS     Spematophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; Vitaceae; Vitis.
            1 (bases 1 to 26)
            Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
            Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.

JOURNAL
COMMENT     Location/Qualifiers
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            /cultivar="Cabernet Sauvignon"
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            /dev_stage="ripening stage"
            /clone_1lb="Ripe Grape Skin Triplex2 Library"
            /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
            SfiIA; Site_2: SfiIB, Oriented library"

FEATURES
source

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spematophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; Vitaceae; Vitis.
1 (bases 1 to 26)
Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..26
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL005C03"
/dev_stage="ripening stage"
/clone_1lb="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB, Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      5393 AAAAAAAAAAAGAAAAA 5415
      ||||| ||||| ||||| |||||
      25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 283
LOCUS      CN545888
DEFINITION EST 17832 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION  CN545888
VERSION     CN545888
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS     Spematophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; Vitaceae; Vitis.
            1 (bases 1 to 26)
            Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
            Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.

JOURNAL
COMMENT     Location/Qualifiers
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            SfiIA; Site_2: SfiIB, Oriented library"

FEATURES
source

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/organism="Vitis vinifera"
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/cultivar="Cabernet Sauvignon"
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/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiIB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 284
CN546608/c 26 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18752 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS58RB008H03 3', mRNA sequence.
ACCESSION CN546608
VERSION CN546608.1 GI:46911233
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 26)
Abbal,P., Agasse,A., Ageorges,A., Aranasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Gilsenat,D., Grimplet,J.,
Hamdi,S., Komieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..26
location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 285
CN546649/c 26 bp mRNA linear EST 30-APR-2004
LOCUS

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DEFINITION EST 18420 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera cDNA clone B3CS37TB007C08 3', mRNA sequence.
ACCESSION CN546649
VERSION CN546649.1 GI:46911274
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 26)
Abbal,P., Agasse,A., Ageorges,A., Aranasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Gilsenat,D., Grimplet,J.,
Hamdi,S., Komieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
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1..26
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007C08"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAAGAAAAA 5415
Db 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 286
AZ342914/c 26 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0076C22P Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0076C22 F, genomic survey sequence.
ACCESSION AZ342914
VERSION AZ342914.1 GI:10420628
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0076 row: C column: 22
 Seq primer: CCGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES

source

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 /sex="Male"
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 /clone_1lb="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 0.3%; Score 18.2; DB 1; Length 26;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAAATC 1202

Db 24 AAGAGAGAGAGAGAGAGCTTC 2

RESULT 287
 AZ359871
 LOCUS 26 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0102H23R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 accession AZ359871
 version 1
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0102 row: H column: 23
 Seq primer: CACACAGGAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES

source

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 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 0.3%; Score 18.2; DB 1; Length 26;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAGAAAAA 5415

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 288
 AZ376664
 LOCUS 26 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0130B08R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 accession AZ376664
 version 1
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: B column: 08
Seq primer: CACACAGGAAACAGCTATAC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"
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/clone="U081M0130E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U081M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;

Best Local Similarity 87.0%; Pred. No. 1.9e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 289

AZ389765

LOCUS 26 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0150D13R Mouse 10kb plasmid U081M library Mus musculus genomic
clone U081M0150D13 R, genomic survey sequence.

ACCESSION

AZ389765

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0130 row: D column: 13
Seq primer: CACACAGGAAACAGCTATAC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source

Location/Qualifiers

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U081M0150D13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U081M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;

Best Local Similarity 87.0%; Pred. No. 1.9e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 290

AZ414673

LOCUS 26 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0189M07F Mouse 10kb plasmid U081M library Mus musculus genomic
clone U081M0189M07 F, genomic survey sequence.

ACCESSION

AZ414673

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Plate: 0189 row: M column: 07
 Seq primer: CGTGTGTAACACGCGCAGT
 Class: plasmid ends
 High quality sequence stcp: 26.
 Location/Qualifiers

FEATURES

source

1..26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0189M07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
 Best Local Similarity 87.0%; Pred. No. 1.9e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 291

AZ593300 26 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0404E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0404E16 R, genomic survey sequence.
 ACCESSION AZ593300
 VERSION AZ593300.1 GI:11715490
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 26)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0404 row: B column: 16

Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stcp: 26.
 Location/Qualifiers

FEATURES

source

1..26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0404E16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
 Best Local Similarity 87.0%; Pred. No. 1.9e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAAAA 5415
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 292

AZ612722 26 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0439E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0439E17 R, genomic survey sequence.
 ACCESSION AZ612722
 VERSION AZ612722.1 GI:11734912
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 26)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0439 row: B column: 17
 Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
source

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0439E17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5415
|||||
Db 26 AAAAAAAAAAAAAAAAAA 4

RESULT 293
AZ624441/c 26 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0463007F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0463007 F, genomic survey sequence.
ACCESSION AZ624441
VERSION AZ624441.1 GI:11746631
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

SOURCE Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0463 row: G column: 07
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends

High quality sequence stop: 26.
Location/Qualifiers
source

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0463007"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5415
|||||
Db 26 AAAAAAAAAAAAAAAAAA 4

RESULT 294
AZ627846/c 26 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0474H08F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0474H08 F, genomic survey sequence.
ACCESSION AZ627846
VERSION AZ627846.1 GI:11750132
KEYWORDS GSS.

ORGANISM Mus musculus (house mouse)

SOURCE Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: H column: 08
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES source

Location/Qualifiers
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0474H08"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 26;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 295
A2635695/C 26 bp DNA 1linear GSS 13-DEC-2000
LOCUS 1M0493G18F Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0493G18 F, genomic survey sequence.

ACCESSION A2635695.1 GI:11757885
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
GSS.
Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0493 row: G column: 18
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

source

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0493G18"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42ny, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 26;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5415
|||||
25 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 296
A2652515 26 bp DNA 1linear GSS 14-DEC-2000
LOCUS 1M0525H15R Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0525H15 R, genomic survey sequence.

ACCESSION A2652515.1 GI:11789108
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
GSS.
Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0525 row: H column: 15
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

source

1. .26
Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0525H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAA 5415
|||||
DB 1 AAAAAAAAAAAAAAAAAA 23

RESULT 297
AZ800453/C 26 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M058023F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUCG2M058023 F, genomic survey sequence.

ACCESSION
AZ800453
VERSION
AZ800453.1 GI:12952583

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0058 row: 0 column: 23

Seq primer: CGTGTAAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

1..26

/organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M058023"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAA 5415
|||||
DB 26 AAAAAAAAAAAAAAAAAA 4

RESULT 298
AZ963974/C 26 bp DNA linear GSS 27-APR-2001
LOCUS
DEFINITION 2M0233N01F Mouse 10kb plasmid UUC2M library Mus musculus genomic
clone UUCG2M0233N01 F, genomic survey sequence.

ACCESSION
AZ963974
VERSION
AZ963974.1 GI:13835201

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0233 row: N column: 01

Seq primer: CGTGTAAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

1..26

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/mol_type="genomic DNA"

/strain="C57BL/6J"
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/clone="UGGCM0233N01"
/sex="Female"
/lab_host="B. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415

DB 26 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 299

TA324D07P

LOCUS T. brucei sheared genomic DNA clone 324d07, forward sequence,
26 bp DNA linear GSS 13-DEC-2000

ACCESSION AL493390

VERSION AL493390.1 GI:11867755

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 26)

AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,

JOURNAL Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

TITLE Melville, S. E., Rajandream, M. A. and Barrett, B. G.

COMMENT Direct Submission

COMMENT Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

COMMENT project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

COMMENT Cambridge CB10 1SA, E-mail: barrett@sanger.ac.uk and

COMMENT nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),

COMMENT Rockville, MD. Genomic DNA isolated from a cloned population of

COMMENT Trypanosoma brucei (TRU927/4 GUTat 10.1) was mechanically sheared

COMMENT to give a tight size distribution (

COMMENT 4 kb). The v + i method used for the library construction is

COMMENT described in detail in Smith, H. and Venter, J. C. (Making small

COMMENT insert libraries for whole genome shotgun sequencing projects. In

COMMENT Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.

COMMENT Barrett, Oxford University Press, 1999).
DETAILS OF T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

1..26
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRU927"

/db_xref="taxon:5691"
/clone="324d07"

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Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAAA 5415

DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 300

BX548564/c

LOCUS BX548564 Glosina morsitans morsitans adult infected gut Glosina
21 bp mRNA linear EST 10-OCT-2003

DEFINITION BX548564 Glosina morsitans morsitans adult infected gut Glosina

ACCESSION BX548564

VERSION BX548564.1 GI:33298798

KEYWORDS EST.

SOURCE Glosina morsitans morsitans

ORGANISM Glosina morsitans morsitans

REFERENCE 1 (bases 1 to 21)

AUTHORS Lehane, M. J., Akroy, S., Gibson, W., Kerhornou, A., Berriman, M.,

TITLE Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.

COMMENT Adult midgut expressed sequence tags from the tsetse fly Glosina

COMMENT morsitans morsitans and expression analysis of putative immune

COMMENT response genes

COMMENT Genome Biol. 4 (10), R63 (2003)

JOURNAL MEDLINE

PUBMED 14519198

COMMENT Contact: Hall N

COMMENT Pathogen Sequencing Unit

COMMENT The Sanger Institute The Wellcome Trust Genome Campus

COMMENT Hinxton, Cambridge, CB10 1SA, UK

COMMENT Request for clones, please contact: Mike Lehane

COMMENT Prof. M. J. Lehane

COMMENT School of Biological Sciences,

COMMENT University of Wales,

COMMENT Bangor LL57 2UW

COMMENT All clones with suffix gic are reverse primer reads starting at 5'

COMMENT end of the cDNA all pic reads are from

COMMENT the 3' end.

Location/Qualifiers

1..21

/organism="Glosina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tset01903_p1c"

/tissue_type="adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with
T. brucei"

Query Match 0.3%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5394 AAAAAAAAAACAAAGAAAAA 5414

DB 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 301

AZ394897/c

LOCUS AZ394897 Mouse 10kb plasmid UGGCM library Mus musculus genomic

DEFINITION clone UGGCM0158H11 R, genomic survey sequence.

ACCESSION A2394897 GI:10509969
 VERSION A2394897.1
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES
 source location/Qualifiers
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 /mol_type="genomic DNA"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gblAF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1200
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 DB 21 AGAGAGAGAGAGAGAGAGA 1

RESULT 302
 A2486776 21 bp DNA linear GSS 05-OCT-2000
 LOCUS A2486776
 DEFINITION 1M0315M10F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 clone UUCG1M0315M10 F, genomic survey sequence.
 ACCESSION A2486776

VERSION A2486776.1 GI:10653882
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: M column: 10
 Seq primer: CTTGTAAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES
 source location/Qualifiers
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 /mol_type="genomic DNA"
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 /clone="UUCG1M0315M10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gblAF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5395 AAAATACAAAAAGAAAAA 5415
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 DB 21 AAAATATAAAAAA 1

RESULT 303
 A2589098 21 bp DNA linear GSS 13-DEC-2000
 LOCUS A2589098
 DEFINITION 1M0397B19R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 clone UUCG1M0397B19 R, genomic survey sequence.
 ACCESSION A2589098
 VERSION A2589098.1 GI:11711288

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0397 row: B Column: 19
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1.21
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/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1200
DB 1 AGAGAGAGAGAGAGAGAGCA 21

RESULT 304
AZ597932/c 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0412D23F Mouse 10kb plasmid UGC1M library Mus musculus genomic
DEFINITION clone UGC1M0412D23 F, genomic survey sequence.
ACCESSION AZ597932
VERSION AZ597932.1 GI:11720122
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0412 row: D Column: 23
Seq primer: CGTTGTAACAGCAGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1.21
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUCG1M0412D23"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5395 AAAATACAAAAGAAAAA 5415
DB 21 AAAAAGAAAAAGAAAAA 1

RESULT 305
AZ627978 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0476104F Mouse 10kb plasmid UGC1M library Mus musculus genomic
DEFINITION clone UGC1M0476104 F, genomic survey sequence.
ACCESSION AZ627978
VERSION AZ627978.1 GI:11750168
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: 1 column: 04
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/clone="UUC1M0476L04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAAA 1200
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Db 21 AGAGAGAGAGAGAGAGAGA 1

RESULT 306
AZ822825
LOCUS AZ822825 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0096120F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUCG2M0096120 F, genomic survey sequence.
ACCESSION AZ822825
VERSION AZ822825.1 GI:12992733
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: 1 column: 20
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5413
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAA 21

RESULT 307
AZ633751
LOCUS AZ633751 22 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M048911F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUCG1M048911 F, genomic survey sequence.
ACCESSION AZ633751
VERSION AZ633751.1 GI:11755941
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

TITLE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0489 row: 1 column: 11
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0489111"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1200
|||||
DB 21 AGAGAGAGAGAGAGAGAGA 1

RESULT 308
LOCUS AZ622888 23 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M009606R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M009606 R, genomic survey sequence.
ACCESSION AZ622888
VERSION AZ622888.1 GI:1292796
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 23)

TITLE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: G column: 06
Seq primer: CACACGAAACGATGAC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M009606"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAA 1200
|||||
DB 2 AGAGAGAGAGAGAGAGAGA 22

RESULT 309
LOCUS AZ627850 24 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0474N20F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0474N20 F, genomic survey sequence.
ACCESSION AZ627850
VERSION AZ627850.1 GI:11750136
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: N column: 20
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0474N20"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 90.5%; Pred. No.1.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy
5393 AAAAAAAAAACAAAAAGAAA 5413
||||| |||||||
4 AAAAAAAAAATAAAAAGAAA 24

Db
4 AAAAAAAAAATAAAAAGAAA 24

RESULT 310
A0247142 25 bp mRNA linear EST 22-APR-2004
LOCUS A0247142 FL Lolium multiflorum cDNA clone F1023C10-5, mRNA
DEFINITION A0247142 FL Lolium multiflorum cDNA clone F1023C10-5, mRNA
sequence.
ACCESSION A0247142
VERSION A0247142.1 GI:46504411
KEYWORDS EST.
SOURCE Lolium multiflorum (Italian ryegrass)
ORGANISM Lolium multiflorum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poaceae; Lolium.
REFERENCE 1 (bases 1 to 25)

AUTHORS
Ikeda,S.
Lolium multiflorum EST Project
Unpublished (2004)

JOURNAL
Contact: Seishi Ikeda
Japan Grassland Farming Forage Seed Association (JFSA)
Forage Crop Research Institute (FCRI)
Higashitakada 388-5, Nishinasuno, Tochigi 329-2742, Japan
Tel: 81-287-37-6755
Fax: 81-287-37-6757
Email: siked67@fjfsas.or.jp
Contact:Tadaaki Takamizo (takamizo@affrc.go.jp)
National Institute of Livestock and Grassland Science, Nishinasuno
Resistance gene analog.

COMMENT
Location/Qualifiers

FEATURES
source
1..25
/organism="Lolium multiflorum"
/mol_type="mRNA"
/db_xref="taxon:4521"
/clone="FL023C10-5"
/tissue_type="Inflorescence"
/clone_lib="PL"

Query Match
Best Local Similarity 90.5%; Pred. No.2e+02; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy
1181 GAGAAAGAGAGAGAGAAAT 1201
||||| |||||||
2 GAGAGAGAGAGAGAGAACT 22

Db
2 GAGAGAGAGAGAGAGAACT 22

RESULT 311
CD028814 25 bp mRNA linear EST 07-MAY-2003
LOCUS CD028814
DEFINITION mgc8009XP04.f.b Magnaporthe grisea CS Uni-Zap XR library Magnaporthe
grisea cDNA clone mgc8009XP04 5', mRNA sequence.
ACCESSION CD028814
VERSION CD028814.1 GI:30410270
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 25)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhattarai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
Unpublished (2002)

JOURNAL
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person;
PCR primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgc8009 row: P column: 04
Seq primer: T3.
Location/Qualifiers

FEATURES
source
1..25
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgc8009XP04"
/sex="Mati-2 hermaphrodite"
/cell_type="conidia"
/clone_lib="Magnaporthe grisea CS Uni-Zap XR library"

/note="Vector: pbluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Confidial library. Point inoculation of Guy11 at center of oatmeal agar plate. Canidia were harvested after two weeks of growth. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phred/rnap version 991019 and trimmed according to pnd files (0.05) and for vector seqs."

Query Match 0.3%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1181 GAGAAAGAGAGAGAGAAAT 1201
DB 2 GAGAGAGAGAGAGAGAGAACT 22

RESULT 312
AZ510124 25 bp DNA 1linear GSS 05-OCT-2000
LOCUS 1M0534K22P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0534K22 F, genomic survey sequence.
ACCESSION AZ510124
VERSION AZ510124.1 GI:10691440
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0354 row: K column: 22
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence sctop: 25.
Location/Qualifiers

FEATURES
source 1.25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0534K22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapored mouse DNA was annealed to adapored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGGAAAGAGAGAGAGAAA 1200
DB 25 AGGAGAGAGAGAGAGAGAGA 5

RESULT 313
AZ659095 25 bp DNA 1linear GSS 14-DEC-2000
LOCUS 1M0536E18P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0536E18 F, genomic survey sequence.
ACCESSION AZ659095
VERSION AZ659095.1 GI:11796241
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0536 row: B column: 18
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence sctop: 25.
Location/Qualifiers

FEATURES
source 1.25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0536E18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 2e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1180 AGAGAAAGAGAGAGAGAAA 1200
|||
Db 3 AGAGAGAGAGAGAGAGAGAGA 23

RESULT 314
AZ664804/c 25 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0545H24P Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0545H24 F, genomic survey sequence.
ACCESSION AZ664804
VERSION AZ664804.1 GI:11801950
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0545 row: H column: 24
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 25.

JOURNAL COMMENT
FEATURES
SOURCE
1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0545H24"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 2e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1180 AGAGAAAGAGAGAGAGAAA 1200
|||
Db 25 AGAGAGAGAGAGAGAGAGAGA 5

RESULT 315
AZ399663/c 24 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0165C10R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0165C10 R, genomic survey sequence.
ACCESSION AZ399663
VERSION AZ399663.1 GI:10514737
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: C column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

JOURNAL COMMENT
FEATURES
SOURCE
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0165C10"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5402 CAAAAAGAAAAATGAAAAATGAA 5425
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Db 24 CAAAAAGAAAAATGAAAAATGAA 1

RESULT 316
AZ514388/c 24 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0361H04P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC1M0361H04 F, genomic survey sequence.
ACCESSION AZ514388
VERSION AZ514388.1 GI:10695704
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: H column: 04
Seq primer: CATTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
Location/Qualifiers

1..24
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361H04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5394 AAAAAATGAAAAAATG 5417
||||| ||||| ||||| ||||| |||||
Db 24 AAAAAAATGAAAAAATG 1

RESULT 317
AZ607198 24 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0429G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC1M0429G03 R, genomic survey sequence.
ACCESSION AZ607198
VERSION AZ607198.1 GI:11729388
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: G column: 03
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES
Location/Qualifiers

1..24
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0429G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5392 TAAATAATACAAAAAGAAAAA 5415
|||||
1 TAAATAAAAAAAAAAAAAAAAAAAA 24

RESULT 318
AZ626101/c 24 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0466J07P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0466J07 F, genomic survey sequence.
ACCESSION AZ626101
VERSION AZ626101.1 GI:11748291
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0466 row: J column: 07
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES
source 1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0466J07"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5396 AAAATACAAAAAGAAAAATGAA 5419
|||||
24 AAAAAGAAAAAAGAAAAAGAA 1

RESULT 319
AZ814559/c 24 bp DNA linear GSS 20-FEB-2001
LOCUS 2K0082P18P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0082P18 F, genomic survey sequence.
ACCESSION AZ814559
VERSION AZ814559.1 GI:12984467
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: P column: 18
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES
source 1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082P18"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

and selected for ampicillin resistance."

Query Match 0.3%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAGA 1198
|||||
DB 19 AGAGAGAGAGAGAGAGAGA 1

RESULT 322
AZ433566/C

LOCUS AZ433566 20 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0219C02R Mouse 10kb plasmid UGCCIM library Mus musculus genomic
clone UGCCIM0219C02 R, genomic survey sequence.

ACCESSION AZ433566
VERSION AZ433566.1 GI:10557579
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0219 row: C column: 02

Seq primer: CACACAGGAAACGCTATACG
Class: plasmid ends
High quality sequence stop: 20.

Location/Qualifiers

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0219C02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAGA 1198
|||||
DB 20 AGAGAGAGAGAGAGAGAGA 2

RESULT 323
AZ492997/C

LOCUS AZ492997 20 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0327K24F Mouse 10kb plasmid UGCCIM library Mus musculus genomic
clone UGCCIM0327K24 F, genomic survey sequence.

ACCESSION AZ492997
VERSION AZ492997.1 GI:10666247
KEYWORDS GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0327 row: K column: 24

Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

Location/Qualifiers

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0327K24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAGA 1198
 |||||
 DB 19 AGAGAGAGAGAGAGAGAGA 1

RESULT 324
 A2770557 20 bp DNA 1linear GSS 16-FEB-2001
 LOCUS A2770557/c 1M0572N08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0572N08 F, genomic survey sequence.
 ACCESSION A2770557
 VERSION A2770557.1 GI:12891863
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Place: 0572 row: N column: 08
 Seq primer: CGTGTAAACGACGCGCGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES
 source 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0572N08"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42uv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

0.3%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAGAGA 1198
 |||||
 DB 19 AGAGAGAGAGAGAGAGAGA 1

RESULT 325
 AJ649983 22 bp mRNA 1linear EST 07-JUL-2004
 LOCUS AJ649983 CSEORAN19 Sus scrofa cDNA clone C0003274_A22, mRNA
 DEFINITION sequence.
 ACCESSION AJ649983
 VERSION AJ649983.1 GI:49326828
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 22)
 AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
 Development of cDNA and EST resources for studying reproduction and
 embryo development in pigs and cattle
 Unpublished (2004)
 CONTACT: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

TITLE Single pass sequencing. Bases called and trimmed with phred
 v0.020425.c. Vector identified by cross match with the -minscore 20
 and -mismatch 12 options. Vector:phuescript11(KS) R. Site1: EcORI
 R. Site2: NotI 5' Seq Primer M13P Normalised library constructed
 from pooled ovaries. Clones available from UK Centre for Functional
 Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
 EH25 9PS, www.afk-genomics.org.
 Location/Qualifiers

FEATURES
 source 1..22
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0003274_A22"
 /tissue_type="ovary"
 /clone_lib="CSEORAN19"
 /note="Vector: phuescript11(KS); Site 1: EcORI; Site 2:
 NotI; Single pass sequencing; Normalised library
 constructed from pooled ovaries"

Query Match 0.3%; Score 17.4; DB 1; Length 22;
 Best Local Similarity 94.7%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 CTGGAGCCGACGACCCCG 49
 |||||
 DB 1 CTGGAGCCGACGACCCCG 19

RESULT 326
 AJ747407 22 bp mRNA 1linear EST 07-JUL-2004
 LOCUS AJ747407 forward - stimulated minus unstimulated macrophage Sus
 DEFINITION scrofa cDNA clone F_C0001825b_A06, mRNA sequence.
 ACCESSION AJ747407
 VERSION AJ747407.1 GI:49917653
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 22)
 AUTHORS Hopwood, P.A., Zhang, F., Lowden, S., Talbot, R., Burt, D., Archibald, A.
 and Dixon, L.
 Development of a porcine cDNA microarray

TITLE Development of a porcine cDNA microarray

JOURNAL Unpublished (2004)
 COMMENT Contact: Hopwood PA
 Dept. of Preclinical Veterinary Sciences
 Royal School for Veterinary Studies
 Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM
 Sequencing was performed by ARK genomics. This clone is available
 from ARK-Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS,
 UK. See www.ark-genomics.org or contact info@arkgenomics.org.

FEATURES

source
 1..22
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9623"
 /clone="F_C0001825b_A06"
 /tissue_type="lung"
 /cell_type="macrophage"
 /clone_lib="forward - stimulated minus unstimulated
 macrophage"

Query Match 0.3%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
 ||||| | ||||| |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 327
 AL038477 22 bp mRNA linear EST 06-UTL-2004
 LOCUS DKF2P566C1646.r1.566 (synonym: hfkcd2) Homo sapiens cDNA clone
 DEFINITION DKF2P566C1646 mRNA sequence.
 ACCESSION AL038477
 AL038477.1 GI:49682139
 EST.
 VERSION Homo sapiens (human)
 KEYWORDS Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 22)
 Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
 Wilmann, S.
 TITLE EST (Ottenwaelder, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contract: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.
 Location/Qualifiers
 1..22
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKF2P566C1646"
 /tissue_type="kidney"
 /dev_stage="fetal"
 /lab_host="X1-2b1ue"
 /clone_lib="566 (synonym: hfkcd2)"
 /note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5391 TTTAAAAATACAAAAAGAAA 5412
 ||||| | ||||| |||||
 Db 1 TTTAAAAA 22

RESULT 328
 AW332181/c 22 bp mRNA linear EST 31-JAN-2000
 LOCUS AW332181
 DEFINITION S5C7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

ACCESSION AW332181
 VERSION AW332181.1 GI:6828538
 KEYWORDS EST.
 SOURCE Pneumocystis carinii
 ORGANISM Pneumocystis carinii
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
 Pneumocystidaceae; Pneumocystis.

REFERENCE 1 (bases 1 to 22)
 Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
 Edman, J.C., Kovacs, J. and Cushion, M.
 TITLE Expressed sequence tags from Pneumocystis carinii
 JOURNAL Unpublished (2000)
 COMMENT Contact: Staben C
 School of Biological Sciences
 University of Kentucky
 101 Morgan Building, University of Kentucky, Lexington, KY
 40506-0225, USA
 Tel: 606 257 2161
 Fax: 606 257 1717
 Email: staben@pop.uky.edu.
 Location/Qualifiers
 1..22
 /organism="Pneumocystis carinii"
 /mol_type="mRNA"
 /db_xref="taxon:4754"
 /lab_host="E. coli"
 /clone_lib="AGS-1"
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
 P. carinii organisms (3x10e9) from a single rat (99-1-6,
 sacrificed on 3/17/99) at Cincinnati VA facilities.
 Trizol extracted RNA. Oligo dt priming, standard
 conditions described by vendor, Stratagene. Further
 details see www.uky.edu/Project/Pneumocystis/

FEATURES

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 /clone_lib="AGS-1"
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
 P. carinii organisms (3x10e9) from a single rat (99-1-6,
 sacrificed on 3/17/99) at Cincinnati VA facilities.
 Trizol extracted RNA. Oligo dt priming, standard
 conditions described by vendor, Stratagene. Further
 details see www.uky.edu/Project/Pneumocystis/

Query Match 0.3%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
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 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 329
 AW332399 22 bp mRNA linear EST 31-JAN-2000
 LOCUS S8A2 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
 DEFINITION AW332399
 ACCESSION AW332399.1 GI:6828756
 EST.
 VERSION Homo sapiens (human)
 KEYWORDS Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
 Pneumocystidaceae; Pneumocystis.

REFERENCE 1 (bases 1 to 22)
 Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
 Edman, J.C., Kovacs, J. and Cushion, M.
 TITLE Expressed sequence tags from Pneumocystis carinii
 JOURNAL Unpublished (2000)
 COMMENT Contact: Staben C
 School of Biological Sciences
 University of Kentucky
 101 Morgan Building, University of Kentucky, Lexington, KY
 40506-0225, USA
 Tel: 606 257 2161
 Fax: 606 257 1717
 Email: staben@pop.uky.edu.
 Location/Qualifiers
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 /organism="Pneumocystis carinii"
 /mol_type="mRNA"
 /db_xref="taxon:4754"
 /lab_host="E. coli"

FEATURES

source
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 /organism="Pneumocystis carinii"
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 /db_xref="taxon:4754"
 /lab_host="E. coli"

/clone lib="AGS-1"
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 P. carlini organisms (3x10e9) from a single rat (59-1-6,
 sacrificed on 3/17/99) at Cincinnati VA facilities.
 Trizol extracted RNA. Oligo dt priming, standard
 conditions described by vendor, Stratagene. Further
 details see www.uky.edu/Project/Pneumocystis/

Query Match 0.3%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAGAAAA 5414

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 330 22 bp mRNA linear EST 15-AUG-2003
 CF299342 7LEAF--03-F06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 LOCUS sativa (japonica cultivar-group) cDNA clone 7LEAF--03-F06, mRNA
 DEFINITION

ACCESSION CF299342 GI:33671103

VERSION CF299342

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 22)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1..22 /organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--03-F06"

/issue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAGAAAA 5414

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 331 22 bp mRNA linear EST 15-AUG-2003
 CF300133 7LEAF--04-G19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 LOCUS sativa (japonica cultivar-group) cDNA clone 7LEAF--04-G19, mRNA
 DEFINITION

sequence.

ACCESSION CF300133 GI:33671894

VERSION CF300133

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 22)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

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/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--04-G19"

/issue_type="leaf"

/dev_stage="7 days after germination"

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAAGAAAA 5414

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 332 22 bp mRNA linear EST 15-AUG-2003
 CF310366 ABF--04-P14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 LOCUS library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 DEFINITION ABF--04-P14, mRNA sequence.

ACCESSION CF310366 GI:33682127

VERSION CF310366

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 22)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1..22 /organism="Oryza sativa (japonica cultivar-group)"

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/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_id="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABP)"
/notes="Vector: PCR4-TOPO, Site_1: EcoRI, Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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RESULT 333
 CP311269/c
 LOCUS DEFINITION 22 bp mRNA linear EST 15-AUG-2001
 ABF--06-G21.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa (Japanica cultivar-group) cDNA clone
 ABF--06-G21, mRNA sequence.
 CP311269
 ACCESSION CP311269.1 GI:33683030
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 EST.
 Oryza sativa (Japanica cultivar-group)
 Oryza sativa (Japanica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhacridae; Oryzaceae; Oryza.
 1 (bases 1 to 22)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 COMMENT
 TITLE
 JOURNAL
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 FEATURES

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FEATURES
Source
Location/Qualifiers
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/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABP)"
/note="vector: pCR4-TOPO. Site_1: EcoRI, leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABF-responsive
element binding transcription factor 3 overexpression
line."

0.3%: Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2,le+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0

5393 AAAAAAATGCAAAAAAGAAAA 5414
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DB

22 AAAAAAAAAAAAAAAAAAAAAA 1

	RESULT 334
	CF311713
LOCUS	22 bp mRNA linear EST 15-AUG-2003
DEFINITION	ABF--07-B13.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--07-B13, mRNA sequence.
ACCESSION	CF311713
VERSION	CF311713.1 GI:3683474
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhatroidaeae; Oryzeae; Oryza.
AUTHORS	1 (bases 1 to 22)
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL	Large-scale Sequencing Analyses of Rice ESTs
COMMENT	Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myoungji University Yongin, Kyeonggi, Korea Tel.: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myoungji.ac.kr.

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FEATURES
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                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_id="ABF3-overexpressing transgenic rice plasmid
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                /note="Vector: pCR4-TOPO; Site 1: EcoRI; leaf was dried
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                    then used for PCR. mRNA was prepared from ABA-responsive
                    element binding transcription factor 3 overexpression
                    line."

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Query Match	0.3%	Score 17.2	DB 1	Length 22
Best Local Similarity	86.4%	Pred. No. 2.1e+02		
Matches 19	Conservative 0	Mismatches 3	Indels 0	Gaps 0
QY	5393	AAAAAAAAATACAAAAAGAAAAA	5414	
DB	1	AAAAAAAAAAAAAAAAAAAAAAAAA	22	
RESULT 335				
LOCUS	CF312498			
DEFINITION	ABF--08-B15.G1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone	22 bp	mRNA	linear
ACCESSION	CF312498			
VERSION	CF312498.1	GI:33684259		
KEYWORDS	EST.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eubartoideae; Oryzaceae; Oryza.			
REFERENCE	1 (bases 1 to 22)			
AUTHORS	Kim,J.-S., Jun,K.-M., Cheong,P.-J., Kim,M.-J., Lee,T.-H., Shin,Y.-C.,			

TITLE
Journal
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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/cultivar="Nackdong"
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/clone_11b="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 336
CP330679/c

LOCUS NACL--06-H22.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--06-H22, mRNA
sequence.

ACCESSION

CP330679.1 GI:33809583

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1. 22
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-H22"
/issue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 30 days"
/lab_host="E.coli DH10B"

FEATURES

source

/clone_11b="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 337

CP33430/c

LOCUS JMT--02-F04.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-F04, mRNA sequence.

ACCESSION

CP33430.1 GI:33815154

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 338

CP334781/c

LOCUS JMT--04-DO5.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-DO5, mRNA sequence.

ACCESSION

CP334781

CP334781

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VERSION      CF334781.1 GI:33817904
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
ORGANISM     Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Euphorbiaceae; Oryzaceae; Oryza.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE        Contact: Nahm B.H.
JOURNAL      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongsin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     Location/Qualifiers
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              methyltransferase overexpression line."
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Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAA 5414
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        22 AAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 339
LOCUS      CF336250
DEFINITION JMT--06-D20.b1 AtUMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--06-D20, mRNA sequence.
ACCESSION  CF336250
VERSION     CF336250.1 GI:33820891
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiaceae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE      Contact: Nahm B.H.
JOURNAL    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongsin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
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            /lab_host="E.coli DH10B"
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            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."
Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
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              /clone="JMT--06-D20"
              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH10B"
              /clone_1lb="AtUMT-overexpressing transgenic rice plasmid
              cDNA library (JMT)"
              /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
              was reverse transcribed and then used for PCR. mRNA was
              prepared from Arabidopsis Jasmonate Carboxyl
              methyltransferase overexpression line."
Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

FEATURES     source
              1..22
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="JMT--06-D20"
              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH10B"
              /clone_1lb="AtUMT-overexpressing transgenic rice plasmid
              cDNA library (JMT)"
              /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
              was reverse transcribed and then used for PCR. mRNA was
              prepared from Arabidopsis Jasmonate Carboxyl
              methyltransferase overexpression line."

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--06-D20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="AtUMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAA 5414
        ||||| ||||| ||||| |||||
        22 AAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 340
LOCUS      CF337580
DEFINITION JMT--08-B11.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--08-B11, mRNA sequence.
ACCESSION  CF337580
VERSION     CF337580.1 GI:33823547
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiaceae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE      Contact: Nahm B.H.
JOURNAL    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongsin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
            1..22
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="JMT--08-B11"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_1lb="AtUMT-overexpressing transgenic rice plasmid
            cDNA library (JMT)"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
            was reverse transcribed and then used for PCR. mRNA was
            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."
Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAACAAAGAAAA 5414
        ||||| ||||| ||||| |||||
        22 AAAAAAAAAAAAAAAAAAAAAA 1

```

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 341
CF338524/c 22 bp mRNA linear EST 18-AUG-2003
LOCUS RCL1-01-P07.g1 Regenerated callus lambda phage CDNA library (RCL1)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P07,
mRNA sequence.
ACCESSION CF338524 GI:33825436
VERSION CF338524.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bharitoidae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39347"
/clone="RCL1--01-P07"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_11b="Regenerated callus lambda phage CDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SctI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SctI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5414
|||||
22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 342
CN545550 22 bp mRNA linear EST 30-APR-2004
LOCUS EST 17494 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA
DEFINITION clone B3CS00RL003005 3', mRNA sequence.
ACCESSION CN545550
VERSION CN545550.1 GI:46910175
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; Vitaceae; Vitis.
1 (bases 1 to 22)
Abbal,P., Agasee,A., Ageorges,A., Atanasova,R., Barrieu,P.,
Couture,C., Dedalechamp,F., Delroch,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.

TITLE
JOURNAL
COMMENT
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourlaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..22
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL003005"
/dev_stage="ripening stage"
/clone_11b="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiIB; Oriented library"

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5414
|||||
22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 343
AZ310066 22 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0018D18R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0018D18 R, genomic survey sequence.
ACCESSION AZ310066 GI:10351682
VERSION AZ310066.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamdi,C.,
Ielam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Rellay,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: D column: 18
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence strop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0018D18"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb1[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5414

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 344

AZ351527

LOCUS 22 bp DNA linear GSS 29-SEP-2000
DEFINITION M0089507R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089507 R, genomic survey sequence.

ACCESSION

AZ351527

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: B column: 07

Seq primer: CACACGGAACAGCATATAC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0089507"

FEATURES

source

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb1[AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5414

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 345

AZ357630

LOCUS 22 bp DNA linear GSS 02-OCT-2000
DEFINITION M0099M15P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099M15 F, genomic survey sequence.

ACCESSION

AZ357630

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0099 row: M column: 15

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0099M15"

/sex="Male"

FEATURES

source

/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414
|||||
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 346
AZ388103 22 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0147N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ388103
VERSION 1
KEYWORDS AZ388103.1 GI:10501811
GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0147 row: N column: 14
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0147N14"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414
|||||
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 347
AZ401908 22 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0168P24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ401908
VERSION 1
KEYWORDS AZ401908.1 GI:10516982
GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: P column: 24
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0168P24"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5414
|||||
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 348
A2424307 22 bp DNA linear GSS 03-OCT-2000
LOCUS 1M020324R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0203A24 R, genomic survey sequence.
ACCESSION A2424307
VERSION A2424307.1 GI:10548320
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0203 row: A column: 24
Seq primer: CACACAGAAACAGCTATGACC
Classes: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0203A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAAA 5414
|||||
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 349
A2428818 22 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0212A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0212A05 R, genomic survey sequence.
ACCESSION A2428818
VERSION A2428818.1 GI:10552831
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0212 row: A column: 05
Seq primer: CACACAGAAACAGCTATGACC
Classes: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0212A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[473214]gb/AP12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACCAAAAAAAAA 5414
DB 22 AAAAAAAAAACCAAAAAAAAA 1

RESULT 350
AZ459654/c 22 bp DNA 1linear GSS 04-OCT-2000
LOCUS 1M0264G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0264G12 R, genomic survey sequence.
ACCESSION AZ459654
VERSION AZ459654.1 GI:10617779
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhuesern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0264 row: G column: 12
Seq primer: CACACGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. 22

FEATURES
source
1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0264G12"
/sex="Male"
/lab_host="R. Colt strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[473214]gb/AP12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACCAAAAAAAAA 5414
DB 22 AAAAAAAAAACCAAAAAAAAA 1

RESULT 351
AZ459654/c 22 bp DNA 1linear GSS 04-OCT-2000
LOCUS 1M0264G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0264G12 R, genomic survey sequence.
ACCESSION AZ459654
VERSION AZ459654.1 GI:10617779
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhuesern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0264 row: G column: 12
Seq primer: CACACGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. 22

FEATURES
source
1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0264G12"
/sex="Male"
/lab_host="R. Colt strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414
|||||
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 352
A2463503/c 22 bp DNA linear GSS 04-OCT-2000
LOCUS A2463503
DEFINITION 1M0272824F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0272824 F, genomic survey sequence.
ACCESSION A2463503
VERSION A2463503.1 GI:10621628
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: E column: 24
Seq primer: CGTGTAAACGACGCCAGT

Classes: plasmid ends
High quality sequence stop: 22.

Location/Qualifiers

1..22

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0272824"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414
|||||
Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 353
A2463652/c 22 bp DNA linear GSS 04-OCT-2000
LOCUS A2463652/c
DEFINITION 1M0272812R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0272812 R, genomic survey sequence.
ACCESSION A2463652
VERSION A2463652.1 GI:10621777
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: E column: 12
Seq primer: CACACAGAAACAGCTATGACC

Classes: plasmid ends
High quality sequence stop: 22.

Location/Qualifiers

1..22

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0272812"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5414
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 354
AZ582403 22 bp DNA linear GSS 13-DEC-2000
LOCUS 1M037415R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0374015 R, genomic survey sequence.

ACCESSION AZ582403
VERSION AZ582403.1 GI:11701249

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

REFERENCE
AUTHORS
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunng@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0374 row: J column: 15
Seq primer: CACACGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0374015"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAGAAAAA 5414
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 355
AZ607658 22 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0430A13F Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0430A13 F, genomic survey sequence.

ACCESSION AZ607658
VERSION AZ607658.1 GI:11729848

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

REFERENCE
AUTHORS
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunng@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0430 row: A column: 13
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.

Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0430A13"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5414
|||||
1 AAAAAAAAAAAAAAAAAAAAA 22

RESULT 356
LOCUS A2654691 22 bp DNA linear GSS 14-DEC-2000
DEFINITION IM0529D05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529D05 F, genomic survey sequence.

ACCESSION A2654691
VERSION A2654691.1 GI:11791837
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 05
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

JOURNAL COMMENT

FEATURES
source
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529D05"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5414
|||||
1 AAAAAAAAAAAAAAAAAAAAA 22

RESULT 357
LOCUS A2760533 22 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0554A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554A24 F, genomic survey sequence.

ACCESSION A2760533
VERSION A2760533.1 GI:12868477
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

JOURNAL COMMENT

FEATURES
source
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554A24"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 358
A2779844/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS A2779844
DEFINITION 2M0016112R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
ACCESSION A2779844
VERSION A2779844
KEYWORDS A2779844.1 GI:12910910
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: 1 column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0016112"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 359
A2785019 22 bp DNA linear GSS 16-FEB-2001
LOCUS A2785019/c
DEFINITION 2M0028504R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
ACCESSION A2785019
VERSION A2785019.1 GI:12921341
KEYWORDS A2785019.1
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: 8 column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0028504"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

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Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAAA 5414
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 360
A2787098/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0033A05F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0033A05 F, genomic survey sequence.

ACCESSION A2787098
VERSION A2787098.1 GI:12925520

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0033 row: A column: 05

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG2M0033A05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAAA 5414
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 361
A2787606/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0034G12P Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0034G12 F, genomic survey sequence.

ACCESSION A2787606
VERSION A2787606.1 GI:12925655

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0034 row: G column: 12

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG2M0034G12"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 362
AZ792704/c 22 bp DNA 1linear GSS 16-FEB-2001
LOCUS 2M0045A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0045A24 F, genomic survey sequence.
ACCESSION AZ792704
VERSION AZ792704.1 GI:12936911
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: A column: 24
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0045A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 363
AZ810674/c 22 bp DNA 1linear GSS 20-FEB-2001
LOCUS 2M0076B19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0076B19 F, genomic survey sequence.
ACCESSION AZ810674
VERSION AZ810674.1 GI:12978158
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: B column: 19
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0076B19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 364
A2820439/c
LOCUS A2820439/c 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0092K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0092K13 R, genomic survey sequence.
ACCESSION A2820439
VERSION A2820439.1 GI:12990443
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,R., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: K column: 13
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0092K13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5414
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 365
A2841661
LOCUS A2841661 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0139118 R, genomic survey sequence.
ACCESSION A2841661
VERSION A2841661.1 GI:13011569
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,R., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: I column: 18
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC2M0139118"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414
|||||
1 AAAAAAAAAAAAAAAAAA 22

Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 366

AZ843514/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

1.22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG2M0142124"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UUCGCM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

1.22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG2M0142124"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UUCGCM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

1.22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG2M0142124"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

Query Match 0.3%; Score 17.2; DB 1; Length 22;

Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5414
|||||
22 AAAAAAAAAAAAAAAAAA 1

Db 22 AAAAAAAAAAAAAAAAAA 1

RESULT 367

AZ946102

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

1.22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG2M0207D13"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UUCGCM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

1.22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG2M0207D13"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UUCGCM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

1.22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG2M0207D13"

/sex="Female"

Query Match 0.3%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAAAA 5414
 ||||| ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 368
 LOCUS TA313B09P 22 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 131b09, forward sequence,
 genomic survey sequence.
 ACCESSION AL464164
 VERSION AL464164.1 GI:11834427
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 22)
 REFERENCE Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Title Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..22
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="131b09"

FEATURES
 source

Query Match 0.3%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAAAA 5414
 ||||| ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 369
 LOCUS TA329F10P 22 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 329f10, forward sequence,
 genomic survey sequence.
 ACCESSION AL482691
 VERSION AL482691.1 GI:11868830
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 22)
 REFERENCE Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Title Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..22
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"

FEATURES
 source

Query Match 0.3%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAAAA 5414
 ||||| ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 370
 LOCUS TA35C12Q/C 22 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 35c12, reverse sequence,
 genomic survey sequence.
 ACCESSION AL454256
 VERSION AL454256.1 GI:11855060
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 22)
 REFERENCE Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Title Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..22
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"

FEATURES
 source

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/strain="TREU927"
/db_xref="taxon:5691"
/clone="35c12"

Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAATCAAAAAAGAAAA 5414
      ||||| ||||| ||||| |||||
      22 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 371
TAS80A07P      22 bp      DNA      1linear      GSS 13-DEC-2000
LOCUS      T. brucei sheared genomic DNA clone 380A07, forward sequence,
DEFINITION      genomic survey sequence.
ACCESSION      AL497713
VERSION      AL497713.1 GI:11873435
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei
ORGANISM      Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE      1 (bases 1 to 22)
AUTHORS      Hall, N., Bowman, S., Lemard, N.J., Doggett, J., Atkin, R.,
      Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
      Melville, S.B., Rajandream, M.A. and Barrell, B.G.
      Direct Submision
      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
      project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
      Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
      nilesanger.ac.uk
      Constructed at the Institute for Genomic Research (TIGR),
      Rockville, MD. Genomic DNA isolated from a cloned population of
      Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
      to give a tight size distribution (
      4 kb). The v + 1 method used for the library construction is
      described in detail in Smith, H. and Venter, J.C. (Making small
      insert libraries for whole genome shotgun sequencing projects. In
      Genome Sequencing: A Practical Approach, eds. W. Vaudin and B.
      Barrell, Oxford University Press, 1999).
      Email: nilesanger@sanger.ac.uk
      Details of T. brucei sequencing at the Sanger Centre are available
      at http://www.sanger.ac.uk/Projects/T_brucei/.
      Location/Qualifiers
        1..22
        /organism="Trypanosoma brucei"
        /mol_type="genomic DNA"
        /strain="TREU927"
        /db_xref="taxon:5691"
        /clone="380A07"

FEATURES
      source

Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAATCAAAAAAGAAAA 5414
      ||||| ||||| ||||| |||||
      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 22

RESULT 372
AG194579      22 bp      DNA      1linear      GSS 06-MAR-2004
LOCUS      Pan troglodytes DNA, clone: RP43-072N05.TU, genomic survey
DEFINITION      sequence.
ACCESSION      AG194579
VERSION      AG194579.1 GI:45226755
KEYWORDS      GSS.
SOURCE      Pan troglodytes (Chimpanzee)
ORGANISM      Pan troglodytes

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```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
REFERENCE      1 (bases 1 to 22)
AUTHORS      Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
      Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
      BAC end sequences of library RP-43
      Unpublished
REFERENCE      2 (bases 1 to 22)
AUTHORS      Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
      Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
      Direct Submision
      Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
      Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
      52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
      (E-mail:redstone@mail.krrib.re.kr URL:http://phs.grc.krrib.re.kr/,
      Tel:82-42-866-7181, Fax:82-42-860-4409)
      Clones are derived from the chimpanzee BAC library RP-43 This BAC
      end was generated during the RAD process and may have higher chance
      of clone tracking errors.
      PRIMERS
      Sequencing: TU
      LIBRARY
      Vector : pBACe3.6
      R.Site 1 : EcoRI
      R.Site 2 : EcoRI.
      Location/Qualifiers
        1..22
        /organism="Pan troglodytes"
        /mol_type="genomic DNA"
        /db_xref="taxon:9598"
        /clone="RP43-072N05.TU"
        /sex="male"
        /cell_type="lymphocytes"
        /clone_lib="RP-43 Chimpanzee Male BAC library"

FEATURES
      source

Query Match      0.3%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAAAAAATCAAAAAAGAAAA 5414
      ||||| ||||| ||||| |||||
      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 22

RESULT 373
AL038397      23 bp      mRNA      1linear      EST 06-JUL-2004
LOCUS      DKFZP566N082_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION      DKFZP566N082, mRNA sequence.
ACCESSION      AL038397
VERSION      AL038397.1 GI:49682109
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1 (bases 1 to 23)
AUTHORS      Oltenevaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
      Wiemann, S.
      EST (Oltenevaelder, et al.)
      Unpublished (1999)
COMMENT      Contact: MIPS
      MIPS
      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
      Location/Qualifiers
        1..23
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFZP566N082"
        /clone_type="kidney"
        /dev_stage="fetal"
        /lab_host="X1-2blue"

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/clone_1ib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAATGAAAA 5421
|||||
2 TACAAAAAGAAAAATGAAAA 23

RESULT 374
AL038592 23 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION DKFZP566G1446.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038592
VERSION AL038592.1 GI:49682166
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 23)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Ostenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
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location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566G1446"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAATGAAAA 5421
|||||
2 TACAAAAAGAAAAATGAAAA 23

RESULT 375
AL038609 23 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION DKFZP566G0946.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038609
VERSION AL038609.1 GI:49682169
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 23)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Ostenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.

FEATURES
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location/Qualifiers
1..23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566G0946"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAATGAAAA 5421
|||||
2 TACAAAAAGAAAAATGAAAA 23

RESULT 376
AL038688 23 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION DKFZP566J0646.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038688
VERSION AL038688.1 GI:49682188
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 23)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Ostenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.

FEATURES
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location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566J0646"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAATGAAAA 5421
|||||
2 TACAAAAAGAAAAATGAAAA 23

RESULT 377
CF300172/c 23 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION CF300172 7LEAF--04-H15.b1 Rice leaf plasmid cDNA library 11 (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-H15, mRNA
sequence.

ACCESSION CF300172
VERSION CF300172.1 GI:33671933
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahmegbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF-04-R15"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf Plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5386 AAGAAATTAATAAATACAAAA 5407
Db 22 AATAATTAATAAATAAATAA 1

RESULT 378
CF332379 23 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-N21.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--08-N21, mRNA
sequence.
ACCESSION CF332379
VERSION CF332379.1 GI:33812983
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahmegbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--08-N21"
/issue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_1lb="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5392 TAAAAAATACAAAAAGAAA 5413
Db 22 TAAAAAATACAAAAAGAAA 1

RESULT 379
A2425710 23 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0205123R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0205123 R, genomic survey sequence.
ACCESSION A2425710
VERSION A2425710.1 GI:10549723
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0205 row: L column: 23
Seq primer: CACACAGAAACACCTATGAC
Clas: plasmid ends
High quality sequence scop: 23.
Location/Qualifiers

FEATURES
source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0205123"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0205123"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATCAAAAAAGAAAA 5414
|||||
Db 2 AAAAAAAAAAAAAAAAAAAAA 23

RESULT 380
AZ447220 23 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION 1M0244E15F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0244E15 F, genomic survey sequence.
ACCESSION
AZ447220
VERSION
AZ447220.1 GI:10598989
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: B column: 15
Seq primer: CGTGTAAACGACGCGCAGT
Class: Plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
Source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0244E15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF128072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5394 AAAAAATCAAAAAAGAAAA 5415
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAA 22

RESULT 381
AZ801003 23 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M0059J16F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0059J16 F, genomic survey sequence.
ACCESSION
AZ801003
VERSION
AZ801003.1 GI:12953326
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: J column: 16
Seq primer: CGTGTAAACGACGCGCAGT
Class: Plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
Source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0059J16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF128072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATTCAGAAAAA 5413
|||||
DB 2 TAAAAAATTCAGAAAAA 23

RESULT 382
LOCUS AZ973926 23 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0248N15P Mouse 10kb plasmid UUGCM library Mus musculus genomic
ACCESSION AZ973926
VERSION AZ973926.1 GI:13845153
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Iselm, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A., and Wright, D., Weles, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: N column: 15
Seq primer: CGTTCGTAACACGCGCACT
Class: plasmid ends
High quality sequence step: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCM0248N15"
/sex="Female"
/lab_host="R. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD29, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1183 GAAAGAGAGAGAGAAATCAG 1204
|||||
DB 23 GAGAGAGAGAGAGAGACAG 2

RESULT 383
LOCUS TA55C06P 23 bp DNA linear GSS 13-DEC-2000
DEFINITION T. Brucei sheared genomic DNA clone 55c06, forward sequence, genomic survey sequence.
ACCESSION AL455778
VERSION AL455778.1 GI:11856729
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
1 (bases 1 to 23)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajadream, M.A., and Barrell, B.G.
DIRECT SUBMISSION
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and nhs@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nhs@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

source
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TRBU927"
/db_xref="taxon:5691"
/clone="55c06"

Query Match 0.3%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATTCAGAAAAA 5414
|||||
DB 2 AAAAAAATTCAGAAAAA 23

RESULT 384
LOCUS CA853764 24 bp mRNA linear EST 01-AUG-2003
DEFINITION B12A03.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
ACCESSION CA853764
VERSION CA853764.1 GI:33390569
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

RESULT 384
LOCUS CA853764 24 bp mRNA linear EST 01-AUG-2003
DEFINITION B12A03.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
ACCESSION CA853764
VERSION CA853764.1 GI:33390569
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 24)

Akharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

JOURNAL

COMMENT

Contact: Akharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharon@ba.ars.usda.gov.

FEATURES

source

1..24

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="B12A03"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="CDNA Peking library 12hr SCN3"

/note="Vector: pBluescript SK-; CDNA clones from mRNA

extracted from roots of soybean cv. Peking 12 hrs after

infection by SCN race 3. These are cloned in pBluescript

SK- phagemid."

Query Match 0.3%; Score 17.2; DB 1; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.3e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAAA 5414

Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 385

CF312319/c

DEFINITION ABF--07-P12.g1 ABF3-overexpressing transgenic rice plasmid CDNA

library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone

ABF--07-P12, mRNA sequence.

ACCESSION CF312319

VERSION CF312319.1 GI:33684080

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 24)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm, B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of BioScience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..24

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--07-P12"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

CDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.3%; Score 17.2; DB 1; Length 24;

Best Local Similarity 86.4%; Pred. No. 2.3e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAAA 5414

Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 386

AZ781101/c

DEFINITION 24 bp DNA linear GSS 16-FEB-2001

2M0019J01P Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC2M0019J01 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0019 row: J column: 01

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0019J01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2282 GTCACAGTACCTCAGAGCA 2303
DB 24 GACCAATGACCCAGAGCA 3

RESULT 387
LOCUS AZ812579 24 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0079A23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ812579
VERSION AZ812579.1 GI:12981965
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Place: 0079 row: A column: 23
Seq primer: CGTGTGAAACGACGCGCACT
Clase: Plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0079A23"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5414
DB 3 AAAAAAAAAAAAAAAAAAAAA 24

RESULT 388
LOCUS CF296213/c 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-H19, mRNA
sequence.
ACCESSION CF296213
VERSION CF296213.1 GI:33665246
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.T., Kim, J.K., Kim, Y.-K. and Nam, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--06-H19"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E. coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: BclRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES

source

Query Match 0.3%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412
DB 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 389
LOCUS AL587602/c 23 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587602 BP Chicken Brain library Gallus gallus cDNA clone
ROS059F08, mRNA sequence.

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ACCESSION   AL587602
VERSION     AL587602.1  GI:13192636
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
ORGANISM    Gallus gallus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
             Phasianinae; Gallus.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Murray, P.
TITLE       BP Chicken Brain Library
JOURNAL     Unpublished (2001)
COMMENT     Contact: Frazer Murray
             Dept. Genomics and Bioinformatics
             Roslin Institute
             Roslin, Midlothian, EH25 9PS, UK
             Tel: +44 (0)131 527 4200
             Fax: +44 (0)131 440 0434
             Email: frazer.murray@dbarc.ac.uk
             GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
             (*6854-
             Seg primer: M13P.
FEATURES    Location/Qualifiers
             1..23
             /organism="Gallus gallus"
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             /clone="ROS059R08"
             /tissue_type="Brain"
             /dev_stage="Unknown"
             /lab_host="DH10B"
             /clone_lib="BP Chicken Brain Library"
             /note="Vector: PSPORI; Site 1: NotI; Site 2: SalI; Cloned
             unidirectionally. Primer: Oligo dT, 5' adaptor sequence:
             5' TCGACCTCGAG 3' ; 3 adaptor sequence: 5'
             GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
             Clontech (*6854-1)"

Query Match      0.3%; Score 16.8; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATTCAGAAAAAGAGAA 5413
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    23 AAAAAAAAAAAAAAAAAAGAGAA 3

RESULT 390
CF297907      23 bp mRNA linear EST 15-AUG-2003
LOCUS         7LEAF--01-B05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION    sativa (japonica cultivar-group) cDNA clone 7LEAF--01-B05, mRNA
sequence.
ACCESSION     CF297907
VERSION       CF297907.1  GI:33669668
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 23)
AUTHORS       Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
             Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
             Genomics and Genetics Institute, Greengene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

ACCESSION   AL587602
VERSION     AL587602.1  GI:13192636
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
ORGANISM    Gallus gallus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
             Phasianinae; Gallus.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Murray, P.
TITLE       BP Chicken Brain Library
JOURNAL     Unpublished (2001)
COMMENT     Contact: Frazer Murray
             Dept. Genomics and Bioinformatics
             Roslin Institute
             Roslin, Midlothian, EH25 9PS, UK
             Tel: +44 (0)131 527 4200
             Fax: +44 (0)131 440 0434
             Email: frazer.murray@dbarc.ac.uk
             GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
             (*6854-
             Seg primer: M13P.
FEATURES    Location/Qualifiers
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             /mol_type="mRNA"
             /db_xref="taxon:9031"
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             /dev_stage="Unknown"
             /lab_host="DH10B"
             /clone_lib="BP Chicken Brain Library"
             /note="Vector: PSPORI; Site 1: NotI; Site 2: SalI; Cloned
             unidirectionally. Primer: Oligo dT, 5' adaptor sequence:
             5' TCGACCTCGAG 3' ; 3 adaptor sequence: 5'
             GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
             Clontech (*6854-1)"

```

```

FEATURES    Location/Qualifiers
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             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:39947"
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             /tissue_type="leaf"
             /dev_stage="7 days after germination"
             /lab_host="E.coli DH10B"
             /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
             /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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             prepared from Arabidopsis thaliana Col-0 whole leaf poly(A)
             methyltransferase overexpression line."

Query Match      0.3%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5393 AAAAAATTCAGAAAAAGAGAA 5415
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    23 AAAAAAAAAAAAAAAAAAGAGAA 1

RESULT 391
CF334077      23 bp mRNA linear EST 18-AUG-2003
LOCUS         JMT--03-D17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION    library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--03-D17, mRNA sequence.
ACCESSION     CF334077
VERSION       CF334077.1  GI:33816466
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 23)
AUTHORS       Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
             Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
             Genomics and Genetics Institute, Greengene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.
FEATURES    Location/Qualifiers
             1..23
             /organism="Oryza sativa (japonica cultivar-group)"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:39947"
             /clone="JMT--03-D17"
             /tissue_type="leaf"
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             cDNA library (JMT)"
             /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
             was reverse transcribed and then used for PCR. mRNA was
             prepared from Arabidopsis thaliana Col-0 whole leaf poly(A)
             methyltransferase overexpression line."

Query Match      0.3%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5393 AAAAAATTCAGAAAAAGAGAA 5415
    ||||| ||||| ||||| |||||
    23 AAAAAAAAAAAAAAAAAAGAGAA 1

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RESULT 394
AZ645254/C
LOCUS
DEFINITION 23 bp DNA 1 linear GSS 14-DEC-2000
1M0510005R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0510005 R, genomic survey sequence.
ACCESSION
AZ645254
VERSION
AZ645254.1 GI:1174572
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: O column: 05
Seq primer: CACACGAAACACGATATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5393 AAAAAATCAAAAAAGAAAAA 5415
|||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 395
AZ970753/C
LOCUS
DEFINITION 23 bp DNA 1 linear GSS 27-APR-2001
2M0244E01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0244E01 F, genomic survey sequence.
ACCESSION
AZ970753
VERSION
AZ970753.1 GI:13841980
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: B column: 01
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC2M0244E01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 841 TCTCCAGCCACCACTCCAC 863
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DB 23 TCACTCCCACTCCACCTCCAC 1

CL693171 23 bp DNA 11near GSS 10-OCT-2004
 LOCUS PRI0160b_B06.2 - PRI0160b.BR (23) Note: Recurring String Mixed
 DEFINITION stage fosmid library of P. pacificus var. California Pristionchus
 pacificus genomic, genomic survey sequence.
 ACCESSION CL693171
 VERSION CL693171.1 GI:50215079
 KEYWORDS GSS.
 SOURCE Pristionchus pacificus
 ORGANISM Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.
 1 (bases 1 to 23)
 Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
 ApplDB: an Acedb database for the nematode satellite organism
 Pristionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 CONTACT: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.
 FEATURES
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 Location/Qualifiers
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 var. California"
 /note="Vector: pBf106-5 Fosmid vector"

Query Match 0.3%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 2.6e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAAAGAA 5411
 Db 1 AAAAAAAAAAAAAA 23

RESULT 397
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 LOCUS AZ489586
 DEFINITION 1M0322C12P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0322C12 F, genomic survey sequence.
 ACCESSION AZ489586
 VERSION AZ489586.1 GI:10659481
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0322 Row: C Column: 12
 Seq primer: CGTTGTAACACACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 FEATURES
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 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0322C12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_11b="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (GI:473214|gb|AF19072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1181 GAGAAAGAGAGAGAGA 1198
 Db 19 GAGAGAGAGAGAGAGA 2

RESULT 398
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 LOCUS AZ983014/c
 DEFINITION 2M0264H02P Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0264H02 F, genomic survey sequence.
 ACCESSION AZ983014
 VERSION AZ983014.1 GI:13854241
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: H column: 02
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

location/Qualifiers

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0264H02"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1180 AGAGAAAGAGAGAGAG 1197
|||||

DB 19 AGAGAGAGAGAGAGAGAG 2

RESULT 399
AZ333204 23 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0062J11F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0062J11 F, genomic survey sequence.
ACCESSION AZ333204
VERSION AZ333204.1 GI:10397591
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS

1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: J column: 11
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES

source

location/Qualifiers

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0062J11"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5256 CAGAGTAAAGTGAAGAGA 5275
|||||

DB 21 CAGAGTGAAGTGAAGAGA 4

RESULT 400
AJ658282 21 bp mRNA linear EST 28-JUN-2004
LOCUS AJ658282 KN277 Sus scrofa cDNA clone C0005212_D02, mRNA sequence.
DEFINITION AJ658282
ACCESSION AJ658282
VERSION AJ658282.1 GI:49342351
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS

1 (bases 1 to 21)
Anderson, S. I., Finlayson, H. A. and Archibald, A. L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross-match with the -minscore 20
and -mismatch 12 options. Vector: pBluescriptII(SK+) R. Site1: ECORI
R. Site2: NotI 5' Seg Primer M13P Normalised library constructed
from pooled early embryos, from 8-cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.airgenomics.org.
location/Qualifiers

FEATURES

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source
1. .21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005212_D02"
/issue_type="embryo"
/clone_1ib="KN277"
/notes="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."

Query Match
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 401
AL0666203 21 bp mRNA linear EST 28-JUN-2004
DEFINITION
AJ666203 CSEORAN09 Sus scrofa cDNA clone C0000033_C15, mRNA
sequence.
AJ666203
VERSION
AJ666203.1 GI:49350654
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 21)
Anderson, S.I., Philayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector: pBluescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.ri.genomics.org.
Location/Qualifiers
1. .21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_C15"
/issue_type="placenta"
/clone_1ib="CSEORAN09"
/notes="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentae."

FEATURES
source
1. .21
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_C15"
/issue_type="placenta"
/clone_1ib="CSEORAN09"
/notes="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentae."

Query Match
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 402
AL048777 21 bp mRNA linear EST 04-SEP-2003
LOCUS
AL048777

```

```

DEFINITION
DKFZ2566N053.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZ2566N053, mRNA sequence.
AL048777
VERSION
AL048777.1 GI:4727848
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 21)
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehler, et al.)
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1. .21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ2566N053"
/issue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

FEATURES
source
1. .21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ2566N053"
/issue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 403
CP282216 21 bp mRNA linear EST 14-AUG-2003
LOCUS
CP282216
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-K01,
mRNA sequence.
CP282216
VERSION
CP282216.1 GI:33659603
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacoidae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="14ETL--09-K01"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"

FEATURES
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1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="14ETL--09-K01"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"

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/clone_11b="Rice etiolated leaf plasmid cDNA library (14ERTL)"
/note="Vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 1 AAAAAAAAAAAAAAAAAAAAA 21

RESULT 404
CP292703/C
LOCUS CP292703 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--01-K01.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--01-K01, mRNA sequence.

ACCESSION CP292703 GI:33661736
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE JOURNAL
COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--01-K01"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_11b="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 405
CP295642/C
LOCUS CP295642 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--05-K20.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--05-K20, mRNA sequence.

ACCESSION CP295642 GI:33664675
VERSION

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--05-K20"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_11b="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 406
CP297615
LOCUS CP297615 21 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--08-J10, mRNA sequence.

ACCESSION CP297615 GI:33666648
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

/db_xref="taxon:39947"
/clone="30DGS--08-J10"
/issue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library I (30DGS)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 407
CF298322/c 21 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-K14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-K14, mRNA sequence.
ACCESSION CF298322 GI:33670083
VERSION CF298322.1 GI:33670083
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriocaridaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 21)
Klm,J.S., Jun,K.M., Cheong,P.J., Klm,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Klm,J.K., Klm,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003).
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-K14"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 408
CF300809/c 21 bp mRNA linear EST 15-AUG-2003
LOCUS CF300809/c
DEFINITION 7LEAF--05-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa (japonica cultivar-group) cDNA clone 7LEAF--05-G20, mRNA sequence.
ACCESSION CF300809.1 GI:33672570
VERSION CF300809
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriocaridaceae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 21)
Klm,J.S., Jun,K.M., Cheong,P.J., Klm,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Klm,J.K., Klm,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003).
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--05-G20"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 409
CF312715 21 bp mRNA linear EST 15-AUG-2003
LOCUS CF312715
DEFINITION ABF--08-J10.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-J10, mRNA sequence.
ACCESSION CF312715 GI:33684476
VERSION CF312715
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriocaridaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 21)
Klm,J.S., Jun,K.M., Cheong,P.J., Klm,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Klm,J.K., Klm,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003).
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

```

source
1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABP--08-J10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABP3-overexpressing transgenic rice plasmid
CDNA library (ABP)"
/note="vector: PCR4-TOPO, Site_1: EcoRI, leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 410
CP316073/c 21 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--05-D16.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-D16, mRNA sequence.
CP316073
ACCESSION CP316073.1 GI:33687834
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-D16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="vector: PCR4-TOPO, Site_1: EcoRI, Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 411
CP326952/c 21 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-D20.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--01-D20, mRNA
sequence.
CP326952
ACCESSION CP326952.1 GI:33802159
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-D20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TOPO, Site_1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 412
CP327391/c 21 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-N18.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--01-N18, mRNA
sequence.
CP327391
ACCESSION CP327391.1 GI:33803041
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharoidae; Oryzae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

```

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers

1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-01-N18"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAA 5413
Db 1 AAAAAAAAAAAAAAAAAAAAA 21

RESULT 413 CF332956 21 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--01-K14.b1 AcJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--01-K14, mRNA sequence.
CF332956
CF332956.1 GI:33814150

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers

1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--01-K14"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AcJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 414 CF338057 21 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--08-M03.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--08-M03, mRNA sequence.
CF338057
CF338057.1 GI:33824485

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers

1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--08-M03"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AcJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAA 5413
Db 1 AAAAAAAAAAAAAAAAAAAAA 21

RESULT 415 CF338522 21 bp mRNA linear EST 18-AUG-2003
LOCUS RCL1--01-P04.g1 Regenerated callus lambda phage cDNA library (RCL1)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P04,
mRNA sequence.
CF338522
CF338522.1 GI:33825432

ACCESSION
VERSION
KEYWORDS
EST.

SOURCE
ORGANISM Oryza sativa (Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..21
/organism="Oryza sativa (Japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39847"
/clone="RCU1-01-P04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_idb="Regenerated callus lambda phage cDNA library (RCU1)"
/note="Vector: pBluescript SK(+), Site_1: SctI, Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SctI and 3' end with XhoI site. cDNA was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match
Best Local Similarity 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 416
CN546489 21 bp mRNA linear EST 30-APR-2004
LOCUS EST 18633 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION cDNA clone B3CS57RB007E11 3', mRNA sequence.
ACCESSION CN546489
VERSION CN546489.1 GI:46911114
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
1 (bases 1 to 21)
Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Gissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr

FEATURES
Seq primer: T7.
source
1..21
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007E11"
/dev_stage="ripe stage"
/clone_idb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match
Best Local Similarity 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAGAAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 417
CN546504 21 bp mRNA linear EST 30-APR-2004
LOCUS EST 18648 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION cDNA clone B3CS57RB007G04 3', mRNA sequence.
ACCESSION CN546504
VERSION CN546504.1 GI:46911129
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
1 (bases 1 to 21)
Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Gissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..21
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007G04"
/dev_stage="ripe stage"
/clone_idb="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

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RESULT 418
LOCUS CNS46595/c 21 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18739 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
ACCESSION CNS46595
CDNA clone B3CS58RB008G02 3', mRNA sequence.
VERSION CNS46595.1 GI:46911220
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosales; Vitaceae; Vitis.
1 (bases 1 to 21)
1 Abbel, P., Agasee, A., Ageorges, A., Atanasova, R., Barileu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Komleu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Université de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
FEATURES
source
1..21
location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008G02"
/dev_stage="ripe stage"
/clone_1fb="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiI; Site_2: SfiI; Oriented library"
Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAAAGAAAA 5413
|||||
21 AAAAAAAAAAAAAAAAAAAAA 1
Db
RESULT 419
LOCUS C0779794 21 bp mRNA linear EST 05-AUG-2004
DEFINITION BL007D B05 6-Day Axotol Tail Blastema (6DAXBL) Ambystoma mexicanum
CDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION C0779794
VERSION C0779794.1 GI:50995774
KEYWORDS EST.
SOURCE Ambystoma mexicanum (axotol)
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 21)
1 Habermann, B., Behn, A.G., Herklitz, S., Volkmer, M., Eckelt, K.,
Pehlke, K., Epperlein, H.H., Schaeckert, H.K., Wiebe, G. and Tanaka, B.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
CDNA libraries
Genome Biol. (2004) In press
Contact: Billy M. Tanaka
Tanaka Lab

```

```

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Dresden
Pfeifenhauserstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL007D row: 05 column: E
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES
source
1..21
location/Qualifiers
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/cisue_type="Tail Blastema"
/cell_type="regenerating tail blastema"
/clone_1fb="6-Day Axotol Tail Blastema (6DAXBL)"
/notes="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;
Unnormalized cDNA plasmid library prepared by invitrogen.
Size fractionated mRNA was polyA+ primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-RNA. Average insert size is 1.67 kb.
TAG_LTB=6DAXBL"
Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAAAGAAAA 5413
|||||
21 AAAAAAAAAAAAAAAAAAAAA 1
Db
RESULT 420
LOCUS AZ317208/c 21 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0035102R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0035102 R, genomic survey sequence.
ACCESSION AZ317208
VERSION AZ317208.1 GI:10365804
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
source
1..21
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035102"
/sex="Male"

```

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5395 AAAAAATACAAAAAGAAAAA 5415
||||| ||||| ||||| |||||

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 421

AZ348593

LOCUS

DEFINITION AZ348593 21 bp DNA linear GSS 29-SEP-2000
1M0085A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0085A13 F, genomic survey sequence.

ACCESSION

AZ348593

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

REFERENCE

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: A column: 13
Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. 21

Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0085A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAAGAAAAA 5413
||||| ||||| ||||| |||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 422

AZ350611

LOCUS

DEFINITION AZ350611 21 bp DNA linear GSS 29-SEP-2000
1M0088C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0088C14 F, genomic survey sequence.

ACCESSION

AZ350611

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS MUSCULUS (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

REFERENCE

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: C column: 14
Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. 21

Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0088C14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413
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1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 423
LOCUS AZ386711 21 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0145016R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0145016 R, genomic survey sequence.
ACCESSION AZ386711 GI:10500411
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: 0 column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source 1.21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145016"
/sex="Male"
/lab_host="B. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 424
LOCUS AZ386794 21 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0145022R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0145022 R, genomic survey sequence.
ACCESSION AZ386794 GI:10500494
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmud, M., Meenen, B., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: 0 column: 22
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source 1.21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145022"
/sex="Male"
/lab_host="B. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 425

AZ389287

LOCUS AZ389287 21 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0149A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0149A13 R, genomic survey sequence.

ACCESSION AZ389287
VERSION AZ389287.1 GI:10502395

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0149 row: A column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0149A13"

/sex="Male"

/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"

/clone_11b="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAAA 5413
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 426

AZ389687

LOCUS AZ389687 21 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0150B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0150B10 R, genomic survey sequence.

ACCESSION AZ389687
VERSION AZ389687.1 GI:10503395

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: B column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0150B10"

/sex="Male"

/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"

/clone_11b="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5413
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 427

AZ406936 21 bp DNA linear GSS 03-OCT-2000
LOCUS IM0176E24F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0176E24 F, genomic survey sequence.

ACCESSION AZ406936
VERSION AZ406936.1 GI:10530949

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
Dunn, D., Moyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0176 row: B column: 24
Seq primer: CGTTGTAACACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. 21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0176E24"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5413
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 428

AZ412739 21 bp DNA linear GSS 03-OCT-2000
LOCUS IM0186D23F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0186D23 F, genomic survey sequence.

ACCESSION AZ412739
VERSION AZ412739.1 GI:10536752

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
Dunn, D., Moyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0186 row: D column: 23
Seq primer: CGTTGTAACACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. 21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0186D23"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

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Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAA 5413
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Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 429
A2412931 21 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0186N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0186N08 R, genomic survey sequence.

ACCESSION A2412931 GI:10536944
VERSION A2412931.1
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0186 row: N column: 08

Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0186N08"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAAA 5413
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 430
A2415029 21 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0189M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0189M07 R, genomic survey sequence.

ACCESSION A2415029 GI:10539042
VERSION A2415029.1
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: M column: 07

Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. 21
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (G1|4732114|9b|AP129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAACAAAGAGAAA 5413
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 431
 AZ465890 21 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0276P07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0276P07 F, genomic survey sequence.

ACCESSION AZ465890
 VERSION AZ465890.1 GI:10624015
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

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 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0276 row: F column: 07
 Seq primer: CATTCTTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

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 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
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 ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (G1|4732114|9b|AP129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAACAAAGAGAAA 5413
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 432
 AZ611116 21 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0436N02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0436N02 R, genomic survey sequence.

ACCESSION AZ611116
 VERSION AZ611116.1 GI:11733306
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

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 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0436 row: N column: 02
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

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 /strain="C57BL/6J"
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 /clone="UUGC1M0436N02"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5413
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 434
AZ611423 21 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION 1M0337E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0437E13 R, genomic survey sequence.

ACCESSION
AZ611423
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0437 row: B column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0437E13"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5413
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 434
AZ615628 21 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION 1M0444M19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0444M19 R, genomic survey sequence.

ACCESSION
AZ615628
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0444 row: M column: 19
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0444M19"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 435
AZ627843/c 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0474H03P Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION Clone UGCGIM0474H03 F, genomic survey sequence.

ACCESSION AZ627843.1 GI:11750129

VERSION GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: H column: 03
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0474H03"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

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Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 436
AZ627845 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0474G11P Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION Clone UGCGIM0474G11 F, genomic survey sequence.

ACCESSION AZ627845.1 GI:11750131

VERSION GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weiss, R.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: G column: 11
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1. 21
/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UGCGIM0474G11"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 437

AZ657727 21 bp DNA linear GSS 14-DEC-2000
LOCUS IM0534B07F Mouse 10Kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0534B07 F, genomic survey sequence.
ACCESSION AZ657727
VERSION AZ657727.1 GI:11794873
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiser,R.
Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0534 row: B column: 07
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1..21
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/strain="C57BL/6J"
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/clone="UUGC1M0534B07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10Kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

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Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5413
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 438

AZ766552 21 bp DNA linear GSS 16-FEB-2001
LOCUS IM0564011F Mouse 10Kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0564011 F, genomic survey sequence.
ACCESSION AZ766552
VERSION AZ766552.1 GI:12883741
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiser,R.
Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: O column: 11
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564011"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10Kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATCAGAAAAAGAAA 5413
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 439

AZ769976 21 bp DNA linear GSS 16-FEB-2001
LOCUS AZ769976
DEFINITION 1M0571111F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0571111 F, genomic survey sequence.

ACCESSION AZ769976
VERSION AZ769976.1 GI:12890681

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0571 row: 1 column: 11

Seq primer: CGTGTGAAAACGACGCCACGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1. 21

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0571111"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_11b="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATCAGAAAAAGAAA 5413
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 440

AZ792613 21 bp DNA linear GSS 16-FEB-2001
LOCUS AZ792613/C
DEFINITION 2M0045M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045M12 F, genomic survey sequence.

ACCESSION AZ792613
VERSION AZ792613.1 GI:12936725

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
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Unpublished (2000)
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: M column: 12

Seq primer: CGTGTGAAAACGACGCCACGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1. 21

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0045M12"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_11b="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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adapted vector DNA, and transformed into

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and selected for ampicillin resistance."

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5401 ACNAAAAAGAAAAATGAAA 5421
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21 ACNAAAAAGAAAAATGAAA 1

RESULT 441
A2793486 21 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0046G18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0046G18 R, genomic survey sequence.

ACCESSION A2793486
VERSION A2793486.1 GI:12938487
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: G column: 18
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0046G18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATTCAAAAAGAAA 5413
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21 AAAAAATTCAAAAAGAAA 1

RESULT 442

A2799327 21 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0056C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0056C09 R, genomic survey sequence.

ACCESSION A2799327
VERSION A2799327.1 GI:12950331
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: C column: 09
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source 1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0056C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAA 5413
 |||||
 1 AAAAAAAAAAAAAAAAAAAAA 21

Db

RESULT 443
 A2810054 21 bp DNA 1linear GSS 20-FEB-2001
 LOCUS 2M0074E19F Mouse 10kb plasmid UUGCM library Mus musculus genomic
 DEFINITION clone UUGCM0074E19 F, genomic survey sequence.
 ACCESSION A2810054
 VERSION A2810054.1 GI:12976935
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddun@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0074 row: B column: 19
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCM0074E19"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

0.3%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAAA 5413
 |||||
 1 AAAAAAAAAAAAAAAAAAAAA 21

Db

RESULT 444
 A2815424 21 bp DNA 1linear GSS 20-FEB-2001
 LOCUS 2M0083H1R Mouse 10kb plasmid UUGCM library Mus musculus genomic
 DEFINITION clone UUGCM0083H1 R, genomic survey sequence.
 ACCESSION A2815424
 VERSION A2815424.1 GI:12985332
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddun@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0083 row: H column: 11
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCM0083H11"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
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 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

0.3%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5413
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 Db 1 AAAAAAAAAAAAAAAAAA 21

RESULT 445
 A2819181 21 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0089110R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0089110 R, genomic survey sequence.
 ACCESSION A2819181
 VERSION A2819181 GI:12989089
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0089 row: 1 column: 10
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

1. 21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0089110"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAA 5413
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 Db 1 AAAAAAAAAAAAAAAAAA 21

RESULT 446
 A2832198 21 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0112P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0112P20 F, genomic survey sequence.
 ACCESSION A2832198
 VERSION A2832198 GI:13002106
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0112 row: P column: 20
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

1. 21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0112P20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 AAAAAAAAAAACAAAAA 21

RESULT 449
A2960063

LOCUS 21 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0228A01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0228A01 F, genomic survey sequence.

ACCESSION A2960063

VERSION A2960063.1 GI:13831290

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0228 row: A column: 01

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0228A01"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5413

|||||

Db 1 AAAAAAAAAAAAAAAAAA 21

RESULT 450

BH000837

LOCUS 21 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0228B02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0228B02 R, genomic survey sequence.

ACCESSION BH000837

VERSION BH000837.1 GI:13872063

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0288 row: O column: 20

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0228B02"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAA 5413

|||||

Db 1 AAAAAAAAAAAAAAAAAA 21

RESULT 451
CF282024/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF282024 22 bp mRNA linear EST 14-AUG-2003
14ETL--09-F13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F13,
mRNA sequence.
CF282024
CF282024.1 GI:33659411
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukariyoc; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3947"
/clone="14ETL--09-F13"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAGAAAAA 5413
|||||
22 AAAAAAAAAAAAAAAAAAAAAA 2

DB 22 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 452
CF298427/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF298427 22 bp mRNA linear EST 15-AUG-2003
7LEAF--01-M24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M24, mRNA
sequence.
CF298427
CF298427.1 GI:33670188
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukariyoc; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3947"
/clone="7LEAF--01-M24"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5395 AAAAAATACAAAAGAAAAA 5415
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21 AAAAAATACAAAAGAAAAA 1

DB 21 AAAAAATACAAAAGAAAAA 1

RESULT 453
CF310486
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CF310486 22 bp mRNA linear EST 15-AUG-2003
ABF--05-C16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-C16, mRNA sequence.
CF310486
CF310486.1 GI:33682247
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukariyoc; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3947"
/clone="ABF--05-C16"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried
for 2hr. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 TTTAAAAATTCAAAAAGAAA 5411
 Db 2 TTTAAAAATTCAAAAAGAAA 22

RESULT 454

CO778290

LOCUS CO778290 22 bp mRNA linear EST 05-AUG-2004
 DEFINITION BL003B.H01 6-Day Axiolotl Tail Blastema (6DaxBL) Ambystoma mexicanum
 CDNA 5' similar to hypothetical protein, mRNA sequence.

ACCESSION

CO778290

VERSION

CO778290.1

KEYWORDS

EST.

SOURCE

ORGANISM

Ambystoma mexicanum (axiolotl)

Ambystoma mexicanum

Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

Ambystoma.

1 (bases 1 to 22)

REFERENCE

AUTHORS

TITLE

Habermaun, B., Behin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
 Penhke, K., Eppelstein, H., Schackert, H.K., Wiede, G., and Tanaka, E.M.
 An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
 expressed sequence tags from embryonic and regenerating blastema
 CDNA libraries

Genome Biol. (2004) In press

JOURNAL

COMMENT

Contact: Eily M. Tanaka

Tanaka Lab

Max Planck Institute of Molecular Cell Biology and Genetics,
 Dresden

Pflorshauerstrasse 108, 01307 Dresden, Germany

Tel: 0049 351 210 2620

Fax: 0049 351 210 1489

Email: tanaka@mpi-cbg.de

Plate: BL003B

Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

Location/Qualifiers

1..22

/organism="Ambystoma mexicanum"

/mol_type="mRNA"

/db_xref="taxon:8296"

/cissue_type="Tail Blastema"

/cell_type="regenerating tail blastema"

/clone_lib="6-Day Axiolotl Tail Blastema (6DaxBL) "

/note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
 Unnormalized cDNA plasmid library prepared by Invitrogen.
 Size fractionated mRNA was polyA+ primed and cloned into
 NotI-SalI site of pCMVSPORT6. Bacterial host is
 EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_LIB=6DaxBL"

TAG_LIB=6DaxBL"

Query Match

Best Local Similarity

Matches

18; Conservative

0; Mismatches

3; Indels

0; Gaps

0;

QY

5393

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)

QY 5393 TTTAAAAATTCAAAAAGAAA 5413
 Db 2 TTTAAAAATTCAAAAAGAAA 22

RESULT 456

AZ374487

LOCUS AZ374487 22 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0127H16F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0127H16 F, genomic survey sequence.

ACCESSION

AZ374487

VERSION

AZ374487.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

Ambystoma.

1 (bases 1 to 22)

REFERENCE

AUTHORS

TITLE

Habermaun, B., Behin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
 Penhke, K., Eppelstein, H., Schackert, H.K., Wiede, G., and Tanaka, E.M.
 An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
 expressed sequence tags from embryonic and regenerating blastema
 CDNA libraries

Genome Biol. (2004) In press

JOURNAL

COMMENT

Contact: Eily M. Tanaka

Tanaka Lab

Max Planck Institute of Molecular Cell Biology and Genetics,
 Dresden

Pflorshauerstrasse 108, 01307 Dresden, Germany

Tel: 0049 351 210 2620

Fax: 0049 351 210 1489

Email: tanaka@mpi-cbg.de

Plate: BL003B

Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/cissue_type="genomic DNA"

/cell_type="genomic DNA"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (914732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

TAG_LIB=6DaxBL"

Query Match

Best Local Similarity

Matches

18; Conservative

0; Mismatches

3; Indels

0; Gaps

0;

QY

5393

TTTTTTTTTTTTTTTTTTTT

TTTTTTTTTTTTTTTTTTTT

TTTTTTTTTTTTTTTTTTTT

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TTTTTTTTTTTTTTTTTTTT

REFERENCE
AUTHORS

1 (bases 1 to 22)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: H column: 16
Seq primer: CGTGTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0127H16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATCAAAAAAGAAA 5413
|||||
Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 457

AZ505769
LOCUS 22 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0346A10R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0346A10 R, genomic survey sequence.
ACCESSION AZ505769
VERSION AZ505769.1 GI:10687085
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0346 row: A column: 10
Seq primer: CACACGAAACGATGAC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0346A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATCAAAAAAGAAA 5413
|||||
Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 458

AZ823875
LOCUS 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0098K07F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0098K07 F, genomic survey sequence.
ACCESSION AZ823875
VERSION AZ823875.1 GI:12993795
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: K column: 07
Seq primer: CGTTGTAAACACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0098K07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy
5393 AAAAAAAAAACAAAAAGAAAA 5413
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 459
AZ845735 22 bp DNA linear GSS 20-FEB-2001
LOCUS AZ845735/c
DEFINITION 2M014507R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M014507 R, genomic survey sequence.
ACCESSION AZ845735
VERSION AZ845735.1 GI:113015643
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: J column: 07
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0145J07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy
5395 AAAAAATCAAAAAAGAAAAA 5415
|||||
22 AAAAAAGCCAAAAA 2

RESULT 460
TA303G05P 22 bp DNA linear GSS 13-DEC-2000
LOCUS TA303G05P
DEFINITION T. brucei sheared genomic DNA clone 303g05, forward sequence.
genomic survey sequence.
ACCESSION AL497383
VERSION AL497383.1 GI:11865504
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 22)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

TITLE Melville, S.B., Rajandream, M.A. and Barrell, B.G.
JOURNAL Direct Submission

COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhls@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nhls@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="303g05"

Query Match 0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5405 AAAAGAAAAATGAAATATAA 5425

1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 461
LOCUS CL693160 22 bp DNA linear GSS 10-JUL-2004
DEFINITION PRI0160a_P09.2 - PRI0160a.BR (32) Note: Recurring String Mixed
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.

ACCESSION CL693160.1 GI:50215068

SOURCE

ORGANISM Pristionchus pacificus
Pristionchus pacificus
Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 22)

REFERENCE Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AUTHORS ApqDB: an AcceDB database for the nematode satellite organism
TITLE Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)

COMMENT

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39 Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Classes: fosmid ends.

FEATURES
source
1..22
Location/Qualifiers

/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBplfos-5 fosmid vector"

Query Match 0.3%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5395 AAAAATACAAAAGAAAAA 5415

1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 462

LOCUS AL048776 23 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZP566N213_r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZP566N213, mRNA sequence.

ACCESSION AL048776
VERSION AL048776.1 GI:4727847
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Mammala, Euteria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gaassenhuber, U. and Wiemann, S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

FEATURES

source

1..23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566N213"
/issue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATACAAAAGAAA 5412

3 TAAAAAATACAAAAGAAA 23

RESULT 463
LOCUS AL587621 23 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587621 BP Chicken Brain library Gallus gallus cDNA clone
ROS059H07, mRNA sequence.

ACCESSION AL587621
VERSION AL587621.1 GI:13192655
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

REFERENCE Archonouria; Aves; Neognathae; Galliformes; Phasianidae;
AUTHORS Murray, F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genetics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434

Email: frazer.murray@berc.ac.uk
GCGGCCCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clonetechn
(*6854-

FEATURES

Seq primer: M13P.
Location/Qualifiers
1..23

/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="R05059H07"
/tissue_type="brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_1ib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCCCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clonetechn (*6854-1)"

Query Match 0.3%; Score 16.2; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5395 AAAAAATACAAAAAGAAAAAT 5416
Db 23 AAAAAAAAAAAAAAAAAAAAAAT 2

RESULT 464
B0590647/c 23 bp mRNA linear EST 06-DEC-2002
DEFINITION S015086-024-018-P17-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-018-P17 5-PRIME, mRNA sequence.

ACCESSION B0590647
VERSION B0590647.1 GI:26120230
KEYWORDS EST.

SOURCE
ORGANISM

Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 23)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfach, M.,
Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, D., Lehrach, H.
and Radclouf, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 23 Std Error: 0.00
Plate: 18 row: P column: 17
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers

FEATURES

source

1..23
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189468"
/db_xref="taxon:161934"
/clone="024-018-P17"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_1ib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;

CDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGGGTCCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-BEET
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5394 AAAAAATACAAAAAGAAAAA 5414
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 465
BX559898/c 23 bp mRNA linear EST 10-OCT-2003
DEFINITION BX559898 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans CDNA clone Tse46d05_p1c, mRNA sequence.

ACCESSION BX559898
VERSION BX559898.1 GI:33367802
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 23)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)

TITLE Glossina morsitans morsitans adult infected gut
JOURNAL MEDLINE 14519198
PUBMED 22881942
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

TITLE All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
Location/Qualifiers

FEATURES

source

1..23
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse46d05_p1c"
/tissue_type="adult infected gut"
/clone_1ib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5401 AAAAAAAGAAAAATGAAGA 5421
Db 22 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 466
LOCUS CF279593/C 23 bp mRNA 1linear EST 14-AUG-2003
DEFINITION 14ETL--05-P06.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-P06,
mRNA sequence.
ACCESSION CF279593
VERSION CF279593.1 GI:33656979
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriocaulaceae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 23)
Klm,J.S., Jun,K.M., Cheong,P.J., Klm,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Klm,J.K., Klm,Y.-K. and Nalm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT Contact: Nalm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3947"
/clone="14ETL--05-P06"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="R.coli DH10B"
/clone_1lb="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5405 AAAAGAAAAATGAAATATA 5425
|||||
Db 22 AAAAGAAAAATGAAATATA 5425

RESULT 467
LOCUS AZ621676 23 bp DNA 1linear GSS 13-DEC-2000
DEFINITION 1M045507F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M045507 F, genomic survey sequence.
ACCESSION AZ621676
VERSION AZ621676.1 GI:11743962
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 1000 Std Error: 0.00
Plate: 0455 row: J column: 07
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M045507"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1|473214|gb|AF19072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5396 AAAATACAAAAAAGAAAAAT 5416
|||||
Db 1 AAAATACAAAAAAGAAAAAT 5416

RESULT 468
LOCUS AZ817623 23 bp DNA 1linear GSS 20-FEB-2001
DEFINITION 2M0087N09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0087N09 F, genomic survey sequence.
ACCESSION AZ817623
VERSION AZ817623.1 GI:12987531
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biometrical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
64112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: N column: 09
Seq primer: CGTGTAAACGACGCCACG
Class: plasmid ends
High quality sequence stop: 23.

FEATURES

Source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCM0087N09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UUGCM library"
/note="Vector: pMD28uv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnarep/>). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repeated with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptorized DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD28 (gill4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptorized mouse DNA was annealed to
adaptorized vector DNA, and transformed into
inducible-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.3%	Score 16.2	DB 1	Length 23
Best Local Similarity	85.7%	Pred. No. 2.8e+02		
Matches 18	Conservative 0	Mismatches 3	Indels 0	Gaps 0

Qy	5396	AAATACAAAAAGAAAAAT	5416
Db	1	AAAAAAAAAAAAAAAAAAT	21

RESULT	LOCUS	DEFINITION	19 bp	mRNA	linear	EST 16-FEB-1999
AI371092/c	AI371092	ca070909.x1 NCI CGAP Brn23 Homo sapiens CDNA clone IMAGE:2043424 3'				
		similar to TR:Q26195 Q26195 PVAL GENE. ;contains Ll.b3 Ll				
		repetitive element ;, mRNA sequence.				

ACCESSION	AI371092
VERSION	AI371092.1
	GI:4149845

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 19)	NCI/NINDS-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap .
	National Cancer Institute	National Institute of Neurological

JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.linnl.gov/dbir/image/image.html

FEATURES

Source

```

1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2043424"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
/clone_1b="NCI C6AP Brn23"
/note="Organ: brain; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGGCGAGCGCGCGCATCTTTTTCGTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Patricia Bonaldi."

```

Query Match	0.3%	Score 15.8;	DB 1;	Length 19;
Best Local Similarity	89.5%	Pred. No. 2.6e+02;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 5403 AAAAAAAAAAATGAAA 5421
||| ||| ||| ||| |||
Db 19 AAGAAGAAAAAGGAAA 1

RESULT	470
AZ654747/c	
LOCUS	
AZ654747	19 bp DNA linear
U0529F08 Mouse 10kb plasmid U0529F08 library Mus musculus genomic clone U0529F08 F, genomic survey sequence.	GSS 14-DEC-2000
DEFINITION	

ACCESSION	AZ654747
VERSION	AZ654747.1
KEYWORDS	GI:11791893
SOURCE	GSS.
	Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
1 (bases 1 to 19)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Rodentia; Sclerogomathi; Muridae; Murinae; Mus

TITLES

**JOURNAL
COMMENT**

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0006
Plate: 0529 row: F column: 08
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends

FEATURES High quality sequence stop: 19.

Location/Qualifiers

1. 19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0529F08"

/sex="Male"

/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent R. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5403 AAAAAAAAAAATGAAA 5421
 |||||
 19 AAAAAAAAAAATGAAA 1

Db 19 AAAAAAAAAAATGAAA 1

RESULT 471

CL693177

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

source

source

source

source

source

source

source

/strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus var. California"
 /note="Vector: pBplfos-5 Fosmid vector"

Query Match 0.3%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5395 AAAAAAAAAAATGAAA 5413
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 1 AAAAAAAAAAATGAAA 19

Db 1 AAAAAAAAAAATGAAA 19

RESULT 472

A2375620

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

source

source

source

source

source

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source

source

source

source

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source

source

source

source

source

source

source

source

source

source

High quality sequence stop: 20.
 Location/Qualifiers
 1. 20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0129A08"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0129 Row: A Column: 08
 Seq primer: CGTGTGAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1. 20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0129A08"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAA 5411
|||||
Db 2 AAAAAATACAAAAAGAA 20

RESULT 473

AZ949997

LOCUS 20 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0213J24R Mouse 10kb plasmid UGCGM library Mus musculus genomic

clone UGCGM0213D24 R, genomic survey sequence.

ACCESSION

AZ949997

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

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JOURNAL

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JOURNAL

COMMENT

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Oy 5393 AAAAAATACAAAAAGAA 5411
|||||
Db 2 AAAAAATACAAAAAGAA 20

RESULT 474

AZ345540/C

LOCUS 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080P05F Mouse 10kb plasmid UGCGM library Mus musculus genomic

clone UGCGM0080P05 F, genomic survey sequence.

ACCESSION

AZ345540

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

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JOURNAL

COMMENT

REFERENCE	1 (bases 1 to 22)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Jellam,H., Longacre,S., Mahmond,M., Meenen,E., Pedersen,T., Relli,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nederhausen,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0028 row: 1 column: 08 Seq primer: CACACAGGAAACAGCTAAGACC Class: plasmid ends High quality sequence stop: 22.
FEATURES	Location/Qualifiers
SOURCE	1..22 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6j" /db_xref="taxon:10090" /clone="UUC2M0028108" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-" /clone_lib="Mouse 10kb plasmid UUC2M library" /note="Vector: PWD42mv; Purified genomic DNA from M. musculus C57BL/6j (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match	0.3%; Score 15.6; DB 1; Length 22;
Best Local Similarity	81.8%; Pred. No. 3.2e+02;
Matches	18; Conservative 0; Indels 4; Gaps 0;
Cy	196 TGCCACAGCCCATCTCCGC 217
Db	 22 TGTTCACACCCCATTACCACTC 1
RESULT 478	
BH000233	22 bp DNA linear GSS 27-APR-2001
LOCUS	
DEFINITION	2M0287I21R Mouse 10kb plasmid UUC2M library Mus musculus genomic
ACCESSION	BH000233
VERSION	BH000233.1 GI:13871459
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 22)

```

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Dival,B., Hamill,C.,
Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0287 row: L column: 21
Seq primer: CACGACGAAACACGCTATGAC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES
source
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cclone="UUC2M0287L21"
/sex="female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/cclone_lib="Mouse 10kb plasmid UUC2M library"
/note="Vector: pMD24nv; Purified genomic DNA from M.
laboratory Mouse DNA Resource
Musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD24 (gil4732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.33; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY 5389 AATTAAAAATACCAAAAAGA 5410
||| ||||| ||||| |||||
1 AAAAAAAAAAAAAAAAAAGA 22
RESULT 479
BG668047/c 18 bp mRNA linear EST 30-APR-2001
LOCUS DRABUA12 Rat DRG library Rattus norvegicus CDNA clone DRABUA12 5',
DEFINITION mRNA sequence.
ACCESSION BG668047
VERSION BG668047.1 GI:13889969
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 18)

```

AUTHORS Xiao, H.S., Huang, Q.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C., Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D., Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.

TITLE Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain

JOURNAL MEDLINE Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

PUBMED 22056133

COMMENT 12060780

Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chc.sh.cn)

PCR PRIMERs
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.

FEATURES

source

1..18
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRABU12"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_1ib="Rat DRG library"

Query Match 0.3%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1178 TCAGAGAAAGAGAGAGA 1194
DB 17 TCAGAGAGAGAGAGAGA 1

RESULT 480
BQ594437 18 bp mRNA linear EST 06-DEC-2002
LOCUS BQ594437
DEFINITION BQ594437-024-024-M20-SP6 MP12-ADIS-024-developing root Beta vulgaris
ACCESSION BQ594437
VERSION BQ594437.1 GI:261234020
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 18)
Hewig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelet, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE 22362189
PUBMED 12472698

Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50823 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mp12-koeln.mpg.de

Insert Length: 18 Std Error: 0.00
Plate: 24 row: M column: 20
Seq. primer: SP6; CATACGATTTAGGTCAGCATATAG.
Location/Qualifiers

FEATURES

source

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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:192416"
/db_xref="taxon:161934"
/clone="024-024-M20"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_1ib="MP12-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: SalI, Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfeldener Saatgut AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.3%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1182 AGAAGAGAGAGAGAGA 1198
DB 1 AGAAGAGATGAGAGAGA 17

RESULT 481
CL436223 19 bp DNA linear GSS 18-MAR-2004
LOCUS CL436223
DEFINITION PST7544-NR.Seg MICE1 Mus musculus genomic clone PST7544-NR.Seg
Similar to Nap11, genomic survey sequence.
ACCESSION CL436223
VERSION CL436223.1 GI:45570812
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Hicks, G.G.
www.Escellis.ca
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3B 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicks@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from
http://140.193.242.7/escdb/public_search_frame.php?PST=PST7544-NR.Seq

Classes: Gene Trap.

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 Bv"
/db_xref="taxon:10090"
/clone="PST7544-NR.Seg"
/sex="Male"

/cell_type="Embryonic stem cell"
/cell_line="D3H (71 Subclone)"
/clone_lib="MIBC1"
/note="Vector: U3Neosyl"

Query Match 0.3%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5357 TATAAATTAAATTTT 5373
|||||
Db 2 TATTAATTAAATTTAT 18

RESULT 482
AZ308846/c 21 bp DNA linear GSS 29-SRP-2000
DEFINITION 1M0012H15F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0012H15 F, genomic survey sequence.

ACCESSION AZ308846
VERSION AZ308846.1 GI:10349246

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,W., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contract: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: H column: 15
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAG 5409
|||||
Db 18 AAAAAAAACAAAAG 2

RESULT 483
AB094448 22 bp mRNA linear EST 01-MAY-2003
LOCUS AB094448
DEFINITION AB094448 lambda Triplex2 rice phloem sap cDNA Oryza sativa
(japonica cultivar-group) cDNA clone PA568, mRNA sequence.

ACCESSION AB094448
VERSION AB094448.1 GI:30307353

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)

REFERENCE

Mano,H., Noguchi,M., Oshima,T., Yoneyama,T., Hayashi,H. and
Fujiwara,T.
Small RNAs detected in the rice phloem sap
Unpublished (2003)
Contact: Hiroyori Mano
Plant Genome Center Co., Ltd
Kannondai-25-2, Tsukuba, Ibaraki 305-0856, Japan
Tel: 81-298-39-4823
Email: hmano@pgcna.co.jp.

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="PA568"
/tissue_type="phloem"
/clone_lib="lambda Triplex2 rice phloem sap cDNA"

Query Match 0.3%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1184 AAGAGAGAGAGAGAA 1200
|||||
Db 5 AAGAGATGAGAGAGAA 21

RESULT 484
AJ666402/c 20 bp mRNA linear EST 28-JUN-2004
LOCUS AJ666402
DEFINITION AJ666402 CSEGRAN09 Sus scrofa cDNA clone C0000033_C23, mRNA
sequence.

ACCESSION AJ666402
VERSION AJ666402.1 GI:49350853

KEYWORDS EST.
SOURCE Sus scrofa (pig)

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 20)

REFERENCE

Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI

JOURNAL

COMMENT

Genomics and Bioinformatics

Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -mnscore 20 and -mismatch 12 options. Vector:pbuascriptii(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.airgenomics.org.

FEATURES

source

1..20
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C000003_C23"
/issue_type="placenta"
/clone_1ib="CSEGRAN09"
/note="Vector: pbuascriptii (KS+); Site 1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 TAAATAATCAAAAAGAA 5412

DB 20 TAAAAAAAAAAAAAAAAA 1

RESULT 485

AL038427 20 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP566A1946_r1 566 (synonym: hfk2) Homo sapiens cDNA clone
DEFINITION DKFZP566A1946, mRNA sequence.
ACCESSION AL038427
VERSION AL038427.1 GI:49682121
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ostenwaelder, et al.)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566A1946"
/issue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfk2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAATAATCAAAAAGAA 5411

DB 1 TAAAAAAAAAAAAAAAAA 20

RESULT 486

AL038429

LOCUS AL038429 20 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZP566A1946_r1 566 (synonym: hfk2) Homo sapiens cDNA clone
ACCESSION AL038429
VERSION AL038429.1 GI:49682123
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ostenwaelder, et al.)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566A1946"
/issue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfk2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAATAATCAAAAAGAA 5411

DB 1 TAAAAAAAAAAAAAAAAA 20

RESULT 487
AL038507 20 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP566D1846_r1 566 (synonym: hfk2) Homo sapiens cDNA clone
DEFINITION DKFZP566D1846, mRNA sequence.
ACCESSION AL038507
VERSION AL038507.1 GI:49682146
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)
Ostenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ostenwaelder, et al.)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566D1846"
/issue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfk2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5391 TTTAAATAATACAAAAGAA 5410
|||||
Db 1 TTTAAAAAAAAAAAAAAAAA 20

RESULT 488
AL038570

LOCUS AL038570 20 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZP566F1746.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566F1746, mRNA sequence.
VERSION AL038570
KEYWORDS AL038570.1 GI:49682159
SOURCE EST.

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 20)

AUTHORS Otenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Otenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
source MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566F1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATACAAAAGAA 5411
|||||
Db 1 TTTAAAAAAAAAAAAAAAAA 20

RESULT 489
AL038576

LOCUS AL038576 20 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZP566F0346.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566F0346, mRNA sequence.
VERSION AL038576
KEYWORDS AL038576.1 GI:49682161
SOURCE EST.

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 20)

AUTHORS Otenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Otenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
source MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

1..20
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="DKFZP566F0346"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5391 TTTAAATAATACAAAAGAA 5410
|||||
Db 1 TTTAAAAAAAAAAAAAAAAA 20

RESULT 490
AL038750

LOCUS AL038750 20 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZP566M1146.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566M1146, mRNA sequence.
VERSION AL038750
KEYWORDS AL038750.1 GI:49682199
SOURCE EST.

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 20)

AUTHORS Otenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Otenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
source MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566M1146"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAAGAA 5412
|||||
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 491
AL038754

LOCUS AL038754 20 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZP566M1346.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566M1346, mRNA sequence.
VERSION AL038754
KEYWORDS AL038754.1 GI:49682201
SOURCE EST.

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 20)

AUTHORS Otenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Otenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
source MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

1..20
/organism="Homo sapiens"
/mol_type="mRNA"

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TITLE      EST (Otteenwælder, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
FEATURES
  source
    1. .20
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="DKFZp566M1346"
      /issue_type="kidney"
      /dev_stage="fetal"
      /lab_host="X1-2blue"
      /clone_1lb="566 (synonym: hfk22)"
      /note="Vector: pMPL1; Site_1: NotI; Site_2: SalI"

Query Match
  Best Local Similarity 85.0%; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAAAAATACAAAAGG 5410
  |||||
  1 TTTAAAAAATACAAAAGG 20

RESULT 492
AL038845 20 bp mRNA linear EST 06-JUL-2004
LOCUS    DKFZp566P1746.r1.566 (synonym: hfk22) Homo sapiens cDNA clone
DEFINITION
ACCESSION AL038845
VERSION    AL038845.1 GI:49682220
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  1 (bases 1 to 20)
  Otteenwælder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
  Wiemann, S.
  EST (Otteenwælder, et al.)
  Unpublished (1999)
  Contact: MIPS
  MIPS
  Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
  Location/Qualifiers
    1. .20
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="DKFZp566P1746"
      /issue_type="kidney"
      /dev_stage="fetal"
      /lab_host="X1-2blue"
      /clone_1lb="566 (synonym: hfk22)"
      /note="Vector: pMPL1; Site_1: NotI; Site_2: SalI"

Query Match
  Best Local Similarity 85.0%; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTTAAAAAATACAAAAGG 5410
  |||||
  1 TTTAAAAAATACAAAAGG 20

RESULT 493
AL587630 20 bp mRNA linear EST 02-MAR-2001
LOCUS    AL587630 BP Chicken Brain Library gallus gallus cDNA clone
DEFINITION
ACCESSION AL587630
  ROS060A07, mRNA sequence.
  ACCESSION AL587630

```

```

VERSION    AL587630.1 GI:13192664
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianinae; Gallus.
  1 (bases 1 to 20)
  1 (bases 1 to 20)
  Murray, P.
  BP Chicken Brain Library
  Unpublished (2001)
  Contact: Frazer Murray
  Dept. Genomics and Bioinformatics
  Roslin Institute
  Roslin, Midlothian, EH25 9PS, UK
  Tel: +44 (0)131 527 4200
  Fax: +44 (0)131 440 0434
  Email: frazer.murray@birc.ac.uk
  GCGGCCGCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
  (*6854-
  Seq primer: M13P.
  Location/Qualifiers
    1. .20
      /organism="Gallus gallus"
      /mol_type="mRNA"
      /db_xref="taxon:9031"
      /clone="ROS060A07"
      /issue_type="Brain"
      /dev_stage="Unknown"
      /lab_host="DH10B"
      /clone_1lb="BP Chicken Brain Library"
      /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned
      unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
      5' TCGACCTGAG 3' ; 3' adaptor sequence: 5'
      GCGGCCGCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
      Clontech (*6854-1)"

Query Match
  Best Local Similarity 85.0%; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5403 AAAAAAGAAAATGAAAT 5422
  |||||
  20 AAAAAAGAAAATGAAAT 1

RESULT 494
AM334823 20 bp mRNA linear EST 31-JAN-2000
LOCUS    S39P5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
DEFINITION
ACCESSION AM334823
VERSION    AM334823.1 GI:6831180
KEYWORDS   EST.
SOURCE     Pneumocystis carinii
ORGANISM   Pneumocystis carinii
  Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
  Pneumocystidaceae; Pneumocystis.
  1 (bases 1 to 20)
  1 (bases 1 to 20)
  Smilian, A.G., Arnold, J., Weise, M., Wunderlich, V., Staben, C.,
  Edman, J.C., Kovacs, J. and Cushion, M.
  Expressed sequence tags from Pneumocystis carinii
  Unpublished (2000)
  Contact: Staben C
  School of Biological Sciences
  University of Kentucky
  101 Morgan Building, University of Kentucky, Lexington, KY
  40506-0225, USA
  Tel: 606 257 2161
  Fax: 606 257 1717
  Email: staben@pop.uky.edu.
  Location/Qualifiers
    1. .20
      /organism="Pneumocystis carinii"

```

/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_1ib="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e5) from a single rat (59-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Total extracted RNA. Oligo dt priming, standard
conditions described by vendor. Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATCAAAAAGAAA 5412
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 495
CF280913 20 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--07-M07.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-M07,
mRNA sequence.
ACCESSION CF280913 GI:33658299
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--07-M07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1ib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATCAAAAAGAAA 5412
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 496
CF282035

LOCUS CF282035 20 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-F19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F19,
mRNA sequence.
ACCESSION CF282035 GI:33659422
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-F19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1ib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATCAAAAAGAAA 5412
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 497
CF282414 20 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--09-019.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-019,
mRNA sequence.
ACCESSION CF282414 GI:33659801
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATCAAAAAGAAA 5412
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 496
CF282035

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1. 20 /organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone_1lb="Rice etiolated leaf plasmid cDNA library

14ESTL"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5412

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 498
CF298018 20 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-D19, mRNA
sequence.

ACCESSION

CF298018 GI:33669779

VERSION

CF298018.1

KEYWORDS

EST.

SOURCE

ORGANISM

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. 20 /organism="Oryza sativa (japonica cultivar-group)"

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/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5389 AATTAAAAATACAAAAA 5408

Db 20 AATCAAAAAAAAAAAAAA 1

RESULT 499
CF299822 20 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-P22, mRNA
sequence.

ACCESSION

CF299822 GI:33671583

VERSION

CF299822.1

KEYWORDS

EST.

SOURCE

ORGANISM

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. 20 /organism="Oryza sativa (japonica cultivar-group)"

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/issue_type="leaf"

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/lab_host="E.coli DH10B"

/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 500
CF301720 20 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--06-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L01, mRNA
sequence.

ACCESSION

CF301720 GI:33673481

VERSION

CF301720.1

KEYWORDS

EST.

SOURCE

ORGANISM

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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Location/Qualifiers

FEATURES
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1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 501
CF302027/c 20 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--07-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C16, mRNA
sequence.

ACCESSION
VERSION CF302027
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

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1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.3%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 502
CF308984/c 20 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--03-A01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--03-A01, mRNA sequence.

ACCESSION
VERSION CF308984
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

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1..20
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried
for 2hrs. Oligo capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABF-responsive
element binding transcription factor 3 overexpression
line."
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Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5389 AATTAAAAAATACAAAAA 5408

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 503
CF310604 20 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-F14, mRNA sequence.

ACCESSION
VERSION CF310604
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contract: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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/cultivar="Nackdong"
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/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABP)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAA 5412
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 504
CFJ13067
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CFJ13067 20 bp mRNA linear EST 15-AUG-2003
HD--01-B02.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-B02, mRNA sequence.
CFJ13067
CFJ13067.1 GI:33684828
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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cDNA library (HD)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAA 5412
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 505
CFJ13569/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CFJ13569 20 bp mRNA linear EST 15-AUG-2003
HD--01-L22.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-L22, mRNA sequence.
CFJ13569
CFJ13569.1 GI:33685330
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contract: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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cDNA library (HD)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAAGAAA 5412
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 506
CF319133/c
LOCUS CF319133 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--09-113.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-113, mRNA sequence.
CF319133
ACCESSION CF319133.1 GI:33690894
VERSION EST.
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Tel: 82 31 330 6193
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
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/clone_1lb="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAAAGAAA 5412
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Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 507
CF321721/c
LOCUS CF321721 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--13-B05.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--13-B05, mRNA sequence.
CF321721
ACCESSION CF321721.1 GI:33693482
VERSION EST.
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAAAGAAA 5412
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 508
CF328565
LOCUS CF328565 20 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-114.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-114, mRNA sequence.
CF328565
ACCESSION CF328565.1 GI:33805376
VERSION EST.
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_1lb="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAAGAAA 5412
 |||||
 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 509
 CF331173/c
 LOCUS 20 bp mRNA linear EST 18-AUG-2003
 DEFINITION 1library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--01-F11, mRNA sequence.

ACCESSION
 VERSION CF331173.1 GI:33814617
 KEYWORDS EST.

SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--01-F11"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AcJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAAGAAA 5412
 |||||
 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 510
 CF331170/c
 LOCUS 20 bp mRNA linear EST 18-AUG-2003
 DEFINITION 1library (JMT) Oryza sativa (japonica cultivar-group) cDNA
 JMT--03-F17, mRNA sequence.

ACCESSION
 VERSION CF331170.1 GI:33816671
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--03-F17"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AcJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAAGAAA 5412
 |||||
 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 511
 CF336525/c
 LOCUS 20 bp mRNA linear EST 18-AUG-2003
 DEFINITION 1library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--06-J21, mRNA sequence.

ACCESSION
 VERSION CF336525.1 GI:33821425
 KEYWORDS EST.

SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"

/db_xref="taxon:39947"
 /clone="JMT--06-J21"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="AtUMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412
 DB 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 512
 CF337494/c 20 bp mRNA linear EST 18-AUG-2003
 LOCUS
 DEFINITION JMT--07-P04.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone
 JMT--07-P04, mRNA sequence.
 CF337494
 VERSION CF337494.1 GI:33823378
 EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 BUKARYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriactoidae; Oryzaceae; Oryza.
 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..20
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--07-P04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="AtUMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412
 DB 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 513
 CN545446/c 20 bp mRNA linear EST 30-APR-2004
 LOCUS
 DEFINITION EST 17390 Green Grape Skin TripleX2 library Vitis vinifera CDNA
 clone B3C006G005C02 3', mRNA sequence.
 CN545446
 VERSION CN545446.1 GI:46910071
 EST.

REFERENCE Vitis vinifera
 AUTHORS Vitis vinifera
 BUKARYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 20)
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)
 CONTACT: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: 17.
 Location/Qualifiers
 1..20
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3C006G005C02"
 /dev_stage="green stage"
 /clone_1lb="Green Grape Skin TripleX2 library"
 /note="Organ: Fruit skin; Vector: Lambda TripleX2; Site 1:
 SfiI, Site 2: SfiI, Oriented library"

FEATURES
 source
 1..20
 Location/Qualifiers
 /organism="Vitis vinifera"
 /mol_type="mRNA"
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 /db_xref="taxon:29760"
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 /dev_stage="green stage"
 /clone_1lb="Green Grape Skin TripleX2 library"
 /note="Organ: Fruit skin; Vector: Lambda TripleX2; Site 1:
 SfiI, Site 2: SfiI, Oriented library"

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412
 DB 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 514
 CN545501/c 20 bp mRNA linear EST 30-APR-2004
 LOCUS
 DEFINITION EST 17445 Green Grape Skin TripleX2 library Vitis vinifera CDNA
 clone B3C006G005H02 3', mRNA sequence.
 CN545501
 VERSION CN545501.1 GI:46910126
 EST.

SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 BUKARYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 20)
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)
 CONTACT: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne

REFERENCE Vitis vinifera
 AUTHORS Vitis vinifera
 BUKARYOTA: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 20)
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)
 CONTACT: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33 - (0)5-57-12-25-50
Fax: 00-33 - (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7
Location/Qualifiers

FEATURES

source

1..20
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3C800G405H02"
/dev_stage="green stage"
/clone_1lb="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
Site_2: SfiIB; Oriented library"

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412
|||||
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 515
T50579/c 20 bp mRNA 1linear EST 06-FEB-1995
DEFINITION yb7d604.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone
IMAGS:77095 5' similar to contains 11 repetitive element, mRNA
sequence.
T50579
T50579.1 GI:652439

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 20)

REFERENCE
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.P., Chapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
Marinis, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rife, L.,
Rohlfing, T., Scheilenberg, K., Soares, M.B., Tan, P., Thierly-Meg, J.,
Trevisan, B., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

COMMENT

PUBMED

MEDLINE

JOURNAL

TITLE

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Source: IMAGB Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGB Consortium (info@image.lnl.gov) for further information.
Seq primer: M13RPI
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:506824"
/db_xref="taxon:9606"
/clone="IMAGB:77095"
/sex="female"

/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_1lb="Stratagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI;
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGACGACG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412
|||||
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 516
AZ307671/c 20 bp DNA 1linear GSS 29-SEP-2000
DEFINITION 1M0009M20R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0009M20 R, genomic survey sequence.
AZ307671
AZ307671.1 GI:10346897

GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Haml, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, B., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: M column: 20
Seq primer: CACACAGCAACACGATACAC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0009M20"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into cells chemically-competent E. coli XL10-Gold (Stratagene) and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAA 5412
|||||
20 AAAAAAAAAAAAAAAAAAAAA 1

Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 517
A2333980 20 bp DNA linear GSS 29-SEP-2000
LOCUS A2333980/c
DEFINITION 1M0063K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0063K10 F, genomic survey sequence.

ACCESSION A2333980
VERSION A2333980.1 GI:10400856
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: K column: 10
Seq primer: CGTGTAAACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0063K10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into cells chemically-competent E. coli XL10-Gold (Stratagene) and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAA 5412
|||||
20 AAAAAAAAAAAAAAAAAAAAA 1

Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 518
A2341237 20 bp DNA linear GSS 29-SEP-2000
LOCUS A2341237
DEFINITION 1M0073G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0073G03 R, genomic survey sequence.

ACCESSION A2341237
VERSION A2341237.1 GI:10417288
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: G column: 03
Seq primer: CACACAGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0073G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No.3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5397 AATATCAAAAAGAAAAAT 5416

Db 1 AAAAAAAAAAAAAAAAAAAT 20

RESULT 519

AZ341530 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0073N21R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0073N21 R, genomic survey sequence.

ACCESSION AZ341530.1 GI:10417873

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhusern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

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84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Place: 0073 row: N column: 21

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0073N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD2nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No.3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAAAGAAA 5412

Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 520

AZ343031 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0076F13F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0076F13 F, genomic survey sequence.

ACCESSION AZ343031.1 GI:10420861

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhusern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Place: 0076 row: F column: 13

Seq primer: CATTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0076F13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD2nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5393 AAAAAATACAAAAAGAAA 5412
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 521
AZ343730/c 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0077E20 F, genomic survey sequence.
ACCESSION AZ343730
VERSION AZ343730.1 GI:10422288
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: B column: 20
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20

TITLE
JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: B column: 20
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20

FEATURES
source
1..20

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0077E20"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5395 AAAAAATACAAAAAGAAA 5414
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 522
AZ351273 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0089B18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0089B18 F, genomic survey sequence.
ACCESSION AZ351273
VERSION AZ351273.1 GI:10430510
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: B column: 18
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20

TITLE
JOURNAL
COMMENT Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: B column: 18
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20

FEATURES
source
1..20

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089B18"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412
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1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 523

AZ357623

LOCUS

DEFINITION

20 bp DNA linear GSS 02-OCT-2000
1M0099A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

AZ357623

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL
COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: A column: 20
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099A20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 524

AZ369734

LOCUS

DEFINITION

20 bp DNA linear GSS 02-OCT-2000
1M0120024F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

AZ369734

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL
COMMENT

Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0120 row: O column: 24
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0120024"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 525

A2386573

LOCUS A2386573 20 bp DNA linear GSS 02-OCT-2000

DEFINITION 1M0145C11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0145C11 R, genomic survey sequence.

ACCESSION A2386573

VERSION A2386573.1 GI:10500273

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0145 row: C column: 11

Seq primer: CACACACGAAACAGCTATAC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145C11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 526

A2396481

LOCUS A2396481 20 bp DNA linear GSS 03-OCT-2000

DEFINITION 1M0161K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0161K02 F, genomic survey sequence.

ACCESSION A2396481

VERSION A2396481.1 GI:10511553

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0161 row: K column: 02

Seq primer: CATTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0161K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

0.3%; Score 15.2; DB 1; Length 20;

QY 5393 AAAAAAAAAACAAAAGAAA 5412
 ||||| ||||| ||||| |||||
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 529
 A2463331 20 bp DNA linear GSS 04-OCT-2000
 LOCUS A2463331/C
 DEFINITION 1M0272006F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0272006 F, genomic survey sequence.
 ACCESSION A2463331
 VERSION A2463331.1 GI:10621456
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0272 row: 0 column: 06
 Seq primer: CGTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0272006"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412
 ||||| ||||| ||||| |||||
 DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 530
 A2477734 20 bp DNA linear GSS 04-OCT-2000
 LOCUS A2477734/C
 DEFINITION 1M0297E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0297E23 F, genomic survey sequence.
 ACCESSION A2477734
 VERSION A2477734.1 GI:10635978
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0297 row: E column: 23
 Seq primer: CGTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0297E23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412


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RESULT 533
A2486787/c
LOCUS      20 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION 1M031523F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315023 F, genomic survey sequence.
ACCESSION  A2486787
VERSION     A2486787.1
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contract: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: D column: 23
Seq primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1..20
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412
DB 20 AAAAAAAAAAAAAAAAAA 1

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RESULT 534
A2498625/c
LOCUS      20 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION 1M0336E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0336E05 F, genomic survey sequence.
ACCESSION  A2498625
VERSION     A2498625.1
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contract: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0336 row: E column: 05
Seq primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source
1..20
location/Qualifiers
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0336E05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412
DB 20 AAAAAAAAAAAAAAAAAA 1

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RESULT 535

LOCUS

AZ514729 20 bp DNA linear GSS 05-OCT-2000

DEFINITION

1M0361B1R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION

clone UGCG1M0361B1R, genomic survey sequence.

VERSION

AZ514729

KEYWORDS

AZ514729.1 GI:10696045

SOURCE

GSS.

ORGANISM

Mus musculus (house mouse)

REFERENCE

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 20)

TITLE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weiss, R.

JOURNAL

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

COMMENT

Unpublished (2000)

CONTACT

Contact: Robert B. Weiss

UNIVERSITY

University of Utah Genome Center

ADDRESS

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL

Tel: 801 585 5606

FAX

Fax: 801 585 7177

EMAIL

Email: ddunn@genetics.utah.edu

INSERT

Insert Length: 10000 Std Error: 0.00

PLATE

Plate: 0361 row: B column: 11

SEQ

Seq primer: CACACAGAAACAGCATATGACC

CLASS

Class: plasmid ends

HIGH

High quality sequence stop: 20.

LOCATION

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol

/mol_type="genomic DNA"

/strain

/strain="C57BL/6J"

/db

/db_xref="taxon:10090"

/clone

/clone="UGCG1M0361B1R"

/sex

/sex="Male"

/lab

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

URL

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

QUERY

Query Match 0.3%; Score 15.2; DB 1; Length 20;

BEST

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

MATCHES

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

5393 AAAAAATCAAAAAAGAAA 5412

DB

1 AAAAAAAAAAAAAAAAAA 20

RESULT

536

AZ579122

LOCUS

AZ579122 20 bp DNA linear GSS 13-DEC-2000

DEFINITION

1M0363G19F Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION

clone UGCG1M0363G19 F, genomic survey sequence.

VERSION

AZ579122

KEYWORDS

AZ579122.1 GI:11693583

SOURCE

GSS.

ORGANISM

Mus musculus (house mouse)

REFERENCE

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 20)

TITLE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weiss, R.

JOURNAL

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

COMMENT

Unpublished (2000)

CONTACT

Contact: Robert B. Weiss

UNIVERSITY

University of Utah Genome Center

ADDRESS

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL

Tel: 801 585 5606

FAX

Fax: 801 585 7177

EMAIL

Email: ddunn@genetics.utah.edu

INSERT

Insert Length: 10000 Std Error: 0.00

PLATE

Plate: 0363 row: G column: 19

SEQ

Seq primer: CGTTCGAAACGACGCGCAGT

CLASS

Class: plasmid ends

HIGH

High quality sequence stop: 20.

LOCATION

Location/Qualifiers

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/organism="Mus musculus"

/mol

/mol_type="genomic DNA"

/strain

/strain="C57BL/6J"

/db

/db_xref="taxon:10090"

/clone

/clone="UGCG1M0363G19"

/sex

/sex="Male"

/lab

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

URL

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

QUERY

Query Match 0.3%; Score 15.2; DB 1; Length 20;

BEST

Best Local Similarity 85.0%; Pred. No. 3.3e+02;

MATCHES

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

5396 AAAAAATCAAAAAAGAAA 5415

DB

1 AAAAAATCAAAAAAGAAA 20

RESULT

537

LOCUS AZ579178 20 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0363F11F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0363F11 F, genomic survey sequence.
ACCESSION AZ579178
VERSION AZ579178.1 GI:11693523
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: F column: 11
Seq primer: CGTGTGAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UGCG1M0363F11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5402 CAAAAAAGAAAATGAAA 5421
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Db 1 CAAAAAAGAAAATGAAA 20

RESULT 538
AZ581208 20 bp DNA linear GSS 13-DEC-2000
LOCUS

DEFINITION IM0369P15R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0369P15 R, genomic survey sequence.
ACCESSION AZ581208
VERSION AZ581208.1 GI:11695991
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: F column: 15
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0369P15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5412
|||||
Db 1 AAAAAATACAAAAAGAA 20

RESULT 539
AZ588011 20 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION IM0396A13F Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION clone accession0396a13 F, genomic survey sequence.
 VERSION AZ588011
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid insets
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 84102, USA
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0396 row: A column: 13
 Seq primer: GGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence atop: 20.
 Location/Qualifiers
 1..20

Query Match	0.3%	Score 15.2	DB 1	Length 20
Best Local Similarity	85.0%	Pred. No. 3.3e+02		
Matches 17	Conservative 0	Mismatches 3	Indels 0	Gaps 0
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Db	1	AAAAAAAAAAAAAAAAAAAAA	20	
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AZ607328				
LOCUS	AZ607328	20 bp	DNA	linear
DEFINITION	1M0429A14R Mouse 10kb plasmid UBC1M library Mus musculus genomic			
	Clone UBC1M0429A14 R, genomic survey sequence.			

FEATURES
 SOURCE
 JOURNAL
 COMMENT
 TITLE
 REFERENCE
 AUTHORS
 ORGANISM
 SOURCE
 KEYWORDS
 VERSION
 ACCESSION

Az607328
 Az607328.1 GI:11729518
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Petersen,T.,
 Rellay,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0429 Row: A Column: 14
 Seq primer: CACACAGCAACACGCTATGACC
 Class: plasmid end
 High quality sequence stop: 20.
 location/Qualifiers
 1..20

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Query Match          0.34; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      5393 AAAAAAAAAACCAAAAAAAAAAGAAA 5412
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Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 20

RESULT 541
A2623155      20 bp      DNA      linear      GSS 13.-DEC-2000
LOCUS      A2623155/C
DEFINITION      JM0460K05R Mouse 10kb plasmid UNGC1M library Mus musculus genomic
clone UNGC1M0460K05 R, genomic survey sequence.
ACCESSION      A2623155

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VERSION AZ623155.1 GI:11745345
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0460 row: K column: 05
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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
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/strain="C57BL/6J"
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/clone="UUCG1M0460K05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412
|||||
DB 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 542
AZ623214/c 20 bp DNA linear GSS 13-DEC-2000
LOCUS IM0460U12R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0460U12 R, genomic survey sequence.
ACCESSION AZ623214
VERSION AZ623214.1 GI:11745404

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0460 row: L column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
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/db_xref="taxon:10090"
/clone="UUCG1M0460L12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412
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DB 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 543
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LOCUS IM0507U18R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0507U18 R, genomic survey sequence.
ACCESSION AZ643992
VERSION AZ643992.1 GI:11772092
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0507 Row: D Column: 18
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stocp: 20.
Location/Qualifiers
1..20
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/strain="C57BL/6J"
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/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5412
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DB 1 AAAAAAAAAAAAAAAAAA 20

RESULT 544
AZ645829
LOCUS AZ645829 20 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0511003R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0511D03 R, genomic survey sequence.
ACCESSION AZ645829
VERSION AZ645829.1 GI:11775703
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 Row: D Column: 03
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stocp: 20.
Location/Qualifiers
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/clone="UUCG1M0511D03"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAAA 5412
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DB 20 AAAAAAAAAAAAAAAAAA 1

RESULT 545
AZ650271
LOCUS AZ650271 20 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0520C21F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0520C21 F, genomic survey sequence.
ACCESSION AZ650271
VERSION AZ650271.1 GI:11784588
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weis
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: C column: 21
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U081M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 546

A2760838

LOCUS A2760838 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M055424R Mouse 10kb plasmid U081M library Mus musculus genomic

clone U081M055424 R, genomic survey sequence.

ACCESSION

A2760838

VERSION A2760838.1 GI:12869112

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weis
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
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/clone_lib="Mouse 10kb plasmid U081M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAAA 5412

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 547

A2764504

LOCUS A2764504 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0560M02R Mouse 10kb plasmid U081M library Mus musculus genomic

clone U081M0560M02 R, genomic survey sequence.

ACCESSION

A2764504

VERSION A2764504.1 GI:12879535

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedermausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0560 row: M column: 02
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAA 5412
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 548
LOCUS A2765211 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0562H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0562H04 F, genomic survey sequence.
ACCESSION A2765211
VERSION A2765211.1 GI:12880970
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islem,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedermausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0562 row: H column: 04
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0562H04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAAGAA 5412
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 549
LOCUS A2772091 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0574A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0574A13 R, genomic survey sequence.
ACCESSION A2772091
VERSION A2772091.1 GI:12895040
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: A column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0574A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAATCAAAAAGAAA 5412
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 550
LOCUS A2779425 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0015M18R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUCG2M0015M18 R, genomic survey sequence.
ACCESSION A2779425
VERSION A2779425.1 GI:12910066
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0015 row: M column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0015M18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAAAAAATCAAAAAGAAA 5412
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 551
LOCUS A2784041 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0026B21F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUCG2M0026B21 F, genomic survey sequence.
ACCESSION A2784041
VERSION A2784041.1 GI:12919375
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von

JOURNAL
COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0055 row: G column: 19
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
SOURCE

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0055G13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5412
|||||
20 AAAAAAAAAAAAAAAAAAAAA 1

Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 554
AZ805163 20 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0066114F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M0066114 F, genomic survey sequence.
ACCESSION AZ805163
VERSION AZ805163.1 GI:12965890
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0066 row: L column: 14
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
SOURCE

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0066114"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5412
|||||
1 AAAAAAAAAAAAAAAAAAAAA 20

Db 1 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 555
AZ806521 20 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0068C08R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M0068C08 R, genomic survey sequence.
ACCESSION AZ806521
VERSION AZ806521.1 GI:12969953
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0068 row: C column: 08
Seq primer: CACACAGAAACGCTATACCC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

1. 20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0068C08"
/sex="Male"
/lab_host="R. Col1 strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAAAGAAA 5412
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 556
AZ806585
LOCUS 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0068C15R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0068C15 R, genomic survey sequence.
ACCESSION AZ806585
VERSION AZ806585.1 GI:12970081
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Butelaeostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0068 row: C column: 15
Seq primer: CACACAGAAACGCTATACCC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0068C15"
/sex="Male"
/lab_host="R. Col1 strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAAAGAAA 5412
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 557
AZ809306
LOCUS 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0073D15F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0073D15 F, genomic survey sequence.
ACCESSION AZ809306
VERSION AZ809306.1 GI:12975468
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Butelaeostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: D column: 15
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

1..20
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U062M0073D15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U062M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAGAA 5412
|||||
DB 1 AAAAAAAAAAAAAAAAAA 20

RESULT 558
AZ810986 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0076120R Mouse 10kb plasmid U062M library Mus musculus genomic
clone U062M0076120 R, genomic survey sequence.
ACCESSION AZ810986
VERSION AZ810986.1 GI:12978793
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
University of Utah
Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: I column: 20
Seq primer: CACACAGGAAACAGCTAGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U062M0076120"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U062M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAGAA 5412
|||||
DB 1 AAAAAAAAAAAAAAAAAA 20

RESULT 559
AZ813908 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0081P21F Mouse 10kb plasmid U062M library Mus musculus genomic
clone U062M0081P21 F, genomic survey sequence.
ACCESSION AZ813908
VERSION AZ813908.1 GI:12983804
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah
University of Utah
Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: F column: 21
Seq primer: CCGTGTAAACGACGCCAGCT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"
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/clone_1fb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 0.3%; Score 15.2; DB 1; Length 20;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAA 5412

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 560

AZ817323

DEFINITION 20 bp DNA linear GSS 20-FEB-2001
2M0086C20R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0086C20 R, genomic survey sequence.

ACCESSION

AZ817323

VERSION AZ817323.1 GI:12987327

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: C column: 20
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers

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/strain="C57BL/6J"
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/clone="UUCG2M0086C20"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 0.3%; Score 15.2; DB 1; Length 20;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAA 5412

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 561

AZ817414

DEFINITION 20 bp DNA linear GSS 20-FEB-2001
2M0086K08R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0086K08 R, genomic survey sequence.

ACCESSION

AZ817414

VERSION AZ817414.1 GI:12987328

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606

Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: K column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

Source

/organism="Mus musculus"
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 /sex="male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid U96C1M library"
 /note="Vector: PBD42n1; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 digested DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PBD42 (g14732114[g]/AF12972.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptorized mouse DNA was annealed to
 adaptorized vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Email: ddumegenetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0086 row: J column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence: step: 20.

FEATURES

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 /clone_id="Mouse 10kb plasmid UTGCM library"
 /note="Vector: pMD42uv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnars/>). The DNA
 was hydrolytically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g11473114[gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

RESULT	562
AZ817467	
LOCUS	AZ817467 20 bp DNA linear GSS 20-FEB-2001
DEFINITION	ZM0086CJLR Mouse 10kb plasmid UUCGM library Mus musculus genomic clone UUCGC2M0086J1 R, genomic survey sequence.
ACCESSION	AZ817467
VERSION	AZ817467.1 GI:12987291
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177

RESULT 563
AZ817608/c

LOCUS 20 bp DNA linear GSS 20-FEB-2001

DEFINITION cclone087X08F Mouse 10kb plasmid U0GC1M library Mus musculus genomic

ACCESSION cclone U0GC2W0087X08 F, genomic survey sequence.

VERSION AZ817608

KEYWORDS AZ817608.1 GI:12987516

ORGANISM GSS.

SOURCE Mus musculus (house mouse)

TITLE Mus musculus

REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Iellam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT University of Utah Genome Center
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00
 Plate: 0087 row: K column: 08
 Seq primer: CCGTGTAAAACGACGGCAGCT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

source

1..20

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 /strain="C57BL/6J"
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 /note="Vector: PMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 564
 A2818489 20 bp DNA 1linear GSS 20-FEB-2001
 LOCUS 2M0088K01R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 DEFINITION clone UUCG2M0088K01 R, genomic survey sequence.
 ACCESSION A2818489
 VERSION A2818489.1 GI:12988397
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00

Plate: 0088 row: K column: 01
 Seq primer: CACACAGAAACGATATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

source

1..20

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 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAAA 5412

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 565
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 LOCUS 2M0089M05F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 DEFINITION clone UUCG2M0089M05 F, genomic survey sequence.
 ACCESSION A2818816
 VERSION A2818816.1 GI:12988724
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0089 row: M column: 05

Seq primer: CGTTGTAAACGACGCCCACT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
SOURCE

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAA 5412
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Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 566
AZ837491 20 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0132K13R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M0132K13 R, genomic survey sequence.
ACCESSION AZ837491
VERSION AZ837491.1 GI:13007399
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0132 row: K column: 13
Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
SOURCE

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/mol_type="genomic DNA"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAAA 5412
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 567
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LOCUS 2M0139H16F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M0139H16 F, genomic survey sequence.
ACCESSION AZ841342
VERSION AZ841342.1 GI:13011250
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: H column: 16
Seq primer: CGTTGTAAACGACGCCCACT
Class: plasmid ends

FEATURES
source
High quality sequence stop: 20.
Location/Qualifiers

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/mol_type="genomic DNA"
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/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Cy 5393 AAAAAAAAAACAAAAGAAA 5412
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 568
AZ841558/C 20 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0139A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0139A10 R, genomic survey sequence.
ACCESSION AZ841558
VERSION AZ841558.1 GI:13011466
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: A column: 10
Seq primer: CACACGAAACACGTATACCC
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High quality sequence stop: 20.

FEATURES
source

Location/Qualifiers
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Cy 5393 AAAAAAAAAACAAAAGAAA 5412
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 569
AZ849506 20 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0150P21 R, genomic survey sequence.
ACCESSION AZ849506
VERSION AZ849506.1 GI:13033596
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACGAAACACGTATACCC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers

source

1. 20

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U062M0150P21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5391 TTAATAAAATACAAAAGA 5410
Db 1 TTAATAAAATACAAAAGA 20

RESULT 570
A2858052 20 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0163003R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUCG2M0163003 F, genomic survey sequence.
ACCESSION A2858052
VERSION A2858052.1 GI:13050813
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: 0 column: 03
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Source 1..20
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="U062M0163003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAGAA 5412
Db 1 AAAAAATACAAAAGAA 20

RESULT 571
A2858419 20 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0163003R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUCG2M0163003 R, genomic survey sequence.
ACCESSION A2858419
VERSION A2858419.1 GI:13051545
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: 0 column: 03
Seq primer: CACACAGAAACAGCTAGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Source 1..20
Location/Qualifiers

/mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0193G23"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUCG2M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATACAAAAGAA 5411
 Db 1 TAAAAAATACAAAAGAA 20

RESULT 572
 LOCUS A2936914 20 bp DNA linear GSS 26-APR-2001
 DEFINITION 2M0193G23R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
 accession A2936914
 version A2936914.1 GI:13795495
 keywords GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0193 row: G column: 23
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"

FEATURES
 source

/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0193G23"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUCG2M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 3.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAATACAAAAGAA 5412
 Db 1 AAAAAAATACAAAAGAA 20

RESULT 573
 LOCUS A2949180/c 20 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0212I02R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
 accession A2949180
 version A2949180.1 GI:13820407
 keywords GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0212 row: I column: 02
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"

FEATURES
 source

[/db_xref=taxon:10990"](#)
[/clone="UGGCM0212102"](#)
[/sex="Female"](#)
[/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"](#)
[/clone_lib="Mouse 10kb plasmid UGGCM library"](#)
[/note="Vector: PMD42nt; Purified genomic DNA from M. musculus C57BL/6J \(female\) was obtained from the Jackson Laboratory Mouse Resource \(<http://www.jax.org/resources/documents/dnares/>\). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gels electrophoresis. Vector DNA was prepared from a derivative of pMD42 \[g1473311\[gB\]AF123072.1\], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold \(Stratagene\) cells and selected for ampicillin resistance."](#)

Query Match	0.3%	Score 15.2	DB 1	Length 20
Best Local Similarity	85.0%	Pred. No. 3.3e+02		
Matches 17	Conservative 0	Mismatches 3	Indels 0	Gaps 0

QY	5393	AAAAAAAAATACAAAAAAAAAGAAA	5412
Db	20	AAAAAAAAAAAAAAAAAAAAAAAAA	1

RESULT 574	AZ963973/c	20 bp	DNA	linear	GSS 27-APR-2001
LOCUS	AZ963973				
DEFINITION	2M0233301P Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0233301 F, genomic survey sequence.				

ACCESSION	AZ963973
VERSION	AZ963973.1
KEYWORDS	GI:13835200
SOURCE	GSS.
	Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE
AUTHORS

Bulanyiota; Mezozoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

Journal
Comment
plasmid inserts
unpublished (2000)
Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT

8412, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 023 Row: J Column: 01
Seq primer: CCGTGTAAATCAGCAGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

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FEATURES location/Qualifiers
source 1. .20
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/mol_type="genomic DNA"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"
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/sclone="tUGC2M0233j01"
 /lab host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone.lib="mouse.10kb plasmid tUGC2M library"
 /note="Vector: PWD42nv. Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 digested DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivativative
 of pMW42 (g1473214[gbl APF29072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.3%	Score 15.2;	DB 1;	length 20;
Best Local Similarity	85.0%	Pred. No. 3.3e+02;		
Matches 17;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

OY	5393	AAAAAAAAATACAAAAAAGAAA	5412
Db	20	AAAAAAAAAAAAAAAAAAAAAA	1

LOCUS	DEFINITION	20 bp DNA	linear	GSS 09-JUL-2004
CL680297	PR10128C G05.2 - PR10128C.BR (20) Note: Recurring String Mixed stage fomuld library of <i>P. pacificus</i> var. <i>California</i> <i>Pflicionchus pacificus</i> genomic, genomic survey sequence.			

ACCESSION	CL680297
VERSION	CL680297.1
KEYWORDS	GI:50187127
SOURCE	GSS.
	<i>Pristionchus pacificus</i>

ORGANISM *Pristionchus pacificus*

REFERENCE
AUTHORS
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 20)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE	ApparD3: an Acedb database for the nematode satellite organism <i>Pristionchus pacificus</i>
JOURNAL	Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT	Contact: Sommer RJ

Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: foamid ends.

FEATURES	Location/Qualifiers
source	1. .20

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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54125"
/clone_id="Mixed stage fosmid library of P. pacificus var. California"
/note="vector: pep1fos-5 Fosmid vector"

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Query match	0.38; Score 15.2; DB 1; Length 20;
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Best Local Similarity 85.0%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5406 AAAAAAAAAAATGAAATATA 5425

Db 20 AAAAAAAAAAAGAAAAAAAAA 1

RESULT 576

AL038582

LOCUS AL038582 21 bp mRNA linear EST 06-UTL-2004

DEFINITION DKFZP566P0946.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038582

VERSION AL038582.1 GI:49682163

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 21)

Ostenweider, B., Obermayer, B., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

EST (Ostenweider, et al.)

Unpublished (1999)

Contact: MIPS

FEATURES

Ingolstaedter Landstr.1, D-85764 Neuberberg, Germany.

Location/Qualifiers

1..21

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZP566P0946"

/cissue_type="Kidney"

/dev_stage="fetal"

/lab_host="X1-2blue"

/clone_1ib="566 (synonym: hfkd2)"

/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5402 CAAAAAAAAAATGAAA 5421

Db 2 CAAAAAAAAAATGAAA 21

RESULT 577

AL038839

LOCUS AL038839 21 bp mRNA linear EST 06-UTL-2004

DEFINITION DKFZP566P1346.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038839

VERSION AL038839.1 GI:49682218

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 21)

Ostenweider, B., Obermayer, B., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

EST (Ostenweider, et al.)

Unpublished (1999)

Contact: MIPS

FEATURES

Ingolstaedter Landstr.1, D-85764 Neuberberg, Germany.

Location/Qualifiers

1..21

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="DKFZP566P1346"
/cissue_type="Kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.3%; Score 15.2; DB 1; Length 21;

Best Local Similarity 85.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5402 CAAAAAAAAAATGAAA 5421

Db 2 CAAAAAAAAAATGAAA 21

RESULT 578

AL587702/c

LOCUS AL587702 21 bp mRNA linear EST 02-MAR-2001

DEFINITION ROS060H09, mRNA sequence.

ACCESSION AL587702

VERSION AL587702.1 GI:13192736

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 21)

Murray, F.

BP Chicken Brain Library

Unpublished (2001)

Contact: Frazer Murray

Dept. Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@bbsrc.ac.uk

GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech

(*6854-

Seq primer: M13P.

FEATURES

source

Location/Qualifiers

1..21

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="ROS060H09"

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/lab_host="DH10B"

/clone_1ib="BP Chicken Brain Library"

/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned

unidirectionally. Primer: Oligo dt. 5' adaptor sequence:

5' TGAAGCTGAG 3', 3' adaptor sequence: 5'

GCGGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from

Clontech (*6854-1)"

Query Match 0.3%; Score 15.2; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5396 AAAAAAAAAAATGAAAAT 5416

Db 21 AAAAAAAAAAATGAAAAT 1

RESULT 579

BX556006

LOCUS BX556006 21 bp mRNA linear EST 10-OCT-2003

DEFINITION BX556006 Glosina morsitans morsitans adult infected gut Glosina

ACCESSION	BX556006	morsitans morsitans cDNA clone Tse24c09_p1c, mRNA sequence.
VERSION	BX556006.1	GI:33379965
KEYWORDS	EST.	
SOURCE	Glossina morsitans morsitans	
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.	
REFERENCE	1 (bases 1 to 21)	
AUTHORS	Lehane,M.J., Aksoy,S., Gibson,W., Kershornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.	
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes	
JOURNAL	Genome Biol. 4 (10), R63 (2003)	
MEDLINE	22881942	
PUBMED	14519198	
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end. Location/Qualifiers 1..21 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /sul_species="morsitans" /db_xref="taxon:37546" /clone="Tse24c09_p1c" /issue_type="adult infected gut" /clone_id="Glossina morsitans morsitans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with T.brucei"	
FEATURES	Source	
Query Match	0.3%; Score 15.2; DB 1; Length 21;	
Best Local Similarity	85.0%; Fred.No.3.4e+02;	
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
CY	5393 AAAAAAAAAAAGAA 5412	
DB	21 AAAAAAAAAAAAAAAA 2	
RESULT 580		
BX558161/c		
DEFINITION	BX558161 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse37a05_p1c, mRNA sequence.	
ACCESSION	BX558161	
VERSION	BX558161.1	GI:33429302
KEYWORDS	EST.	
SOURCE	Glossina morsitans morsitans	
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.	
REFERENCE	1 (bases 1 to 21)	
AUTHORS	Lehane,M.J., Aksoy,S., Gibson,W., Kershornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.	
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes	
JOURNAL	Genome Biol. 4 (10), R63 (2003)	
MEDLINE	22881942	

```

PUBMED
COMMENT      14519198
              Contact: Hall N
              Pathogen Sequencing Unit
              The Sanger Institute The Wellcome Trust Genome Campus
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J.Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW
              All clones with suffix gtc are reverse primer reads starting at 5'
              end of the cDNA all plc reads are from
              the 3' end.

FEATURES
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    location/Qualifiers
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            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /db_species="morsitans"
            /db_xref="taxon:37546"
            /clone="T8e37a05_plc"
            /issue_type="adult infected gut"
            /clone_idb="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucel"

Query Match
Best Local Similarity   0.3%; Score 15.2; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5401 AAAAAAAAAAATAATGAA 5420
DB      21 AAAAAAAAAAAAAAAAAAAAA 2
          ||||| ||||| |||
CP276638      21 bp mRNA linear EST 14-NUG-2003
LOCUS       14ETL--01-N19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION   Oryza sativa [japonica cultivar-group] CDNA clone 14ETL--01-N19,
             mRNA sequence.
ACCESSION   CP276638
VERSION     CP276638.1 GI:33654024
KEYWORDS    EST.
SOURCE      Oryza sativa [japonica cultivar-group]
ORGANISM    Oryza sativa [japonica cultivar-group] Embryophyta; Tracheophyta;
             Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae;
             Eupharbioidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 21)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,U.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyonggi, Korea
            Tel.: 82 31 350 6193
            Fax: 82 31 321 6355
            Email: bhnah@gbio.com, bhnah@bio.myongji.ac.kr.
FEATURES
source
    location/Qualifiers
        1..21
            /organism="Oryza sativa [japonica cultivar-group]"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
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            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_idb="Rice etiolated leaf plasmid cDNA library
            (14ETL)"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412
|||||
20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 582
CF311914/c 21 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--07-G07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
1library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-G07, mRNA sequence.

ACCESSION CF311914 GI:33683675
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF--07-G07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABF-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412
|||||
20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 583
CF318152/c 21 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION HD--08-C11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
1library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-C11, mRNA sequence.
ACCESSION CF318152

VERSION CF318152.1 GI:33689913
EST.

KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-C11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_1lb="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAAA 5412
|||||
21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 584
CF319122/c 21 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION HD--09-I07.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
1library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-I07, mRNA sequence.

ACCESSION CF319122 GI:33690883
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
Location/Qualifiers

```

source
1. 21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="HD--09-107"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone.lib="OesDACL1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/notes="vector: PCR4-TOPO, Site_1: EcoRI, Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5406 AAGAGAAAATCGAAATATAA 5425
Db      21 AACGAAAAAATAATAA 2

RESULT 585
A2346717/c      21 bp      DNA      linear      GSS 29-SEP-2000
LOCUS      1M0082002F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0082002 F, genomic survey sequence.
ACCESSION      A2346717
VERSION      A2346717.1 GI:10425954
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: O column: 02
Seq primer: CGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
source
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0082002"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PMP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

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was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5401 ACAAAAAGAAAATGAAA 5420
Db      21 AAAAAAGAAAGAAAGAAA 2

RESULT 586
A2461824      21 bp      DNA      linear      GSS 04-OCT-2000
LOCUS      1M0267B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0267B23 R, genomic survey sequence.
ACCESSION      A2461824
VERSION      A2461824.1 GI:10619949
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: B column: 23
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0267B23"
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/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PMP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5412
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 587
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DEFINITION 1M0328C11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ493766
VERSION AZ493766.1 GI:10667750
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Haml, C., Iselin, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Moose whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymer Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0328 row: C column: 11
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
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1. 21
Location/Qualifiers
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/clone="UUGC1M0328C11"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5392 TAAAAAATACAAAAAGAA 5411
Db 2 TAAAAAAAAAAAAAAAAA 21

RESULT 588
LOCUS CL693165 21 bp DNA linear GSS 10-JUL-2004
DEFINITION PR10160a.G10.2 - PR10160a.BR (21) Note: Recurring string Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL693165
VERSION CL693165.1 GI:50215073
KEYWORDS GSS.

SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Sriivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
APPDB: an Acids database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)

JOURNAL Contact: Sommer RJ
COMMENT Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1. 21
Location/Qualifiers
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_1lb="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pBg1fos-5 Fosmid vector"

Query Match 0.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5389 AATTAATAATACAAAAA 5408
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 589
AZ381798/c

LOCUS	AZ281798	19 bp	DNA	linear	GENS 02-OCT-2000
DEFINITION	IM0138G01R Mouse 10kb plasmid tUSGCM library. Mus musculus genomic clone tUSGCM0138G01 R, genomic survey sequence.				
ACCESSION	AZ281798				
VERSION	AZ281798.1	GI:10495498			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murine; Mus.				
AUTHORS	1 (bases 1 to 19) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isalam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellay, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weis University of Utah Department of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0138 row: G column: 01 Seq primer: CACACAGGAACAGCATGACAC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1..19				
FEATURES					
SOURCE	1..19				

1. 19
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/db_xref="taxon:10090"
/clone="U08101.138061"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid U08101 library"
/note="Vector: PMD449; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (gi|4732111|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.3%	Score 15;	DB 1;	Length 19;
Best Local Similarity	100.0%	Pred. No. 3.3e+02;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1270	CCCCACCA	CCCCA	1284
Db	18	CCCCACCA	CCCCA	4

RESULT 590			
AM248747/C			
LOCUS	19 bp	mRNA	linear
AM248747			EST 07-JAN-2000

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
2821119.sp prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:282119 3'	AM248747	AM248747.1	GI:6591740	EST.	Homo sapiens (human)
mRNA sequence.					Homo sapiens
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
					Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
					1 (bases 1 to 19)
					NIH-MGC http://mgc.nci.nih.gov/.
					National Institutes of Health, Mammalian Gene Collection (MGC)
					Unpublished (1999)
					Other ESTs: 2821119.Sp prime
					Contact: Robert Strausberg, Ph.D.
					Email: cgapbs-remail.nih.gov
					Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling
					Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
					Consortium (LNLN) DNA Sequencing by: Berkeley MGC sequencing
					project Clone distribution: MGC clone distribution information can
					be found through the I.M.A.G.E. Consortium/LNLN at:
					www.bio.lnl.gov/bdnp/image/image.html Base Calling / Quality
					Scores: PHRED from University of Washington Genome Center. Vector
					Trimming: cross_match from University of Washington Genome Center
					PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
					Drosophila Genome Project. University of Washington Genome Center:
					http://www.genome.washington.edu Low Quality Sequence: 7 contiguous
					PHRED high quality bases following vector sequence. Very low
					Quality Sequence: trace file contained 19 contiguous distinct peaks
					following vector sequence. Polyadenylation: Based upon the presence
					of a XhoI site followed by a run of 14 or more T residues at the
					beginning of the sequence, this cDNA insert was polyadenylated.
					Plate: tLCMS row: P column: 16
					High quality sequence stop: 7.
					Location/Qualifiers
					1..19

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1. 19
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="IMAGE:2821119"
   /tissue_type="small cell carcinoma"
   /cell_line="MGC3"
   /lab_host="DH10B (phage-resistant)"
   /clone_id="NH_MGC_7"
   /note="Organ: lung; Vector: pOT7; Site 1: XhoI; Site 2:
   EcoRI; cDNA made by oligo-dT priming. Directionally
   cloned into EcoRI/XhoI sites using the following 5'
   adaptor: GCACGAG(G). Size-selected >500bp for average
   insert size 1.8kb. library constructed by Ling Hong in
   the laboratory of Gerald M. Rubin (University of
   California, Berkeley) using ZAP-cDNA synthesis kit
   (Stratagene) and Superscript II RT (Life Technologies)."

```

Query Match	0.3%	Score 14.8	DB 1	Length 19
Best Local Similarity	88.9%	Pred. No. 3.4e+02		
Matches 16	Conservative 0	Mismatches 2	Indels 0	Gaps 0

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QY      5393 AAAAAAATACAAAAAGA 5410
          |||||
Db      18 AAAAAAATAAAAAAA 1
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RESULT 591

LOCUS	Size	Accession
CRJ334610	19 bp	EST 18-Aug-2003
DEFINITION	JMT-03-p13.b1 A/JMT-overexpressing transgenic rice plasmid cDNA library (JMT) <i>Oryza sativa</i> (japonica cultivar-group) cDNA clone JMT-03-p13, mRNA sequence.	

ACCESSION	CP334610
VERSION	CP334610.1
KEYWORDS	GI:33817556
SOURCE	EST.
ORGANISM	<i>Oryza sativa</i> (japonica cultivar-group)
	<i>Oryza sativa</i> (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacridae; Oryzaceae; Oryza.

1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiyar="Nackdong"
/db_xref="taxon:39847"
/clone="UMT--03-P13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ATUMT-overexpressing transgenic rice plasmid cDNA library (UMT)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5398 AATACAAAGAAAAA 5415
18 AATTAAGAAAAA 1

RESULT 592
AZ345795 19 bp DNA linear GSS 29-SRP-2000
LOCUS 1M0080H09R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0080H09 R, genomic survey sequence.
ACCESSION AZ345795
VERSION AZ345795.1 GI:10425032
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,B.R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 09
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends

JOURNAL
COMMENT

High quality sequence stop: 19.
location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0080H09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PWD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent B. coli XL10-gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5391 TTTAAAAAATCAAAAA 5408
1 TTTAAAAA 18

RESULT 593
AZ513919 19 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0360B13F Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0360B13 F, genomic survey sequence.
ACCESSION AZ513919
VERSION AZ513919.1 GI:10695235
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,B.R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: B column: 13
Seq primer: CATTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 19.

JOURNAL
COMMENT

FEATURES
source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0360E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5403 AAAAAAGAAAAATGAAA 5420
|||||
18 AAAAAAGAAAAAAA 1

Db 18 AAAAAAGAAAAAAA 1

RESULT 594
AZ650252 19 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0520N17F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0520N17 F, genomic survey sequence.
ACCESSION AZ650252
VERSION AZ650252.1 GI:11784550
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: N column: 17
Seq primer: CGTTGTAACGACGCGCAGCT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

source
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0520N17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5398 AATACAAAGAAAAA 5415
|||||
1 AATACAAAGAAAAA 18

Db 1 AATACAAAGAAAAA 18

RESULT 595
AZ650575 19 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0520P13R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0520P13 R, genomic survey sequence.
ACCESSION AZ650575
VERSION AZ650575.1 GI:11785200
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: P column: 13
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5391 TTTAAAAATACAAAAA 5408
DB 1 TTTAAAAATACAAAAA 18

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0520P13"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

RESULT 596
LOCUS AZ766990 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0564H19R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0564H19 R, genomic survey sequence.
ACCESSION AZ766990
VERSION AZ766990.1 GI:12884624
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiser,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0564 row: H column: 19
Seq primer: CACACGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"

Query Match
Best Local Similarity 88.9%; Score 14.8; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5403 AAAAAAGAAAAAATGAAA 5420
DB 2 AAAAAAGAAAAAATGAAA 19

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0564H19"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

RESULT 597
LOCUS AM333777 20 bp mRNA linear EST 31-JAN-2000
DEFINITION S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AM333777
VERSION AM333777.1 GI:6830134
KEYWORDS EST.
SOURCE Pneumocystis carinii
Pneumocystis carinii
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 20)
Smilian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staden,C., Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
JOURNAL Contact: Staden C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY 40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staden@pop.uky.edu.
Location/Qualifiers
1. 20
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_1lb="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI; P. carinii organisms (3x10e6) from a single rat (59-1-6, sacrificed on 3/17/99) at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"

FEATURES
source


```

/cisue.type="kidney"
/dev.stages="fetal"
/lab.host="xl-2blue"
/clone.lib="566 (synonym: hfxd2)"
/notes="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match      0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5391 TTTAAAAAATACAAAAA 5408
Db      3 TTTAAAAAATACAAAAA 20

RESULT 601
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LOCUS      1M0420H13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0420H13 R, genomic survey sequence.
ACCESSION      AZ602152
VERSION      AZ602152.1 GI:11724342
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL      Contact: Robert B. Weiss
COMMENT      University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0420 row: H column: 13
            Seq primer: CACACAGAAACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
            Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0420H13"
                /sex="Male"
                /lab_host="R. Col1 strain XL10-Gold, T1-resistant, F-"
                /clone.lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: pMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and

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purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5397 AATACCAAAAGAAAA 5414
Db      20 AATACCAAAATAAAAA 3

RESULT 602
AZ610868/c      21 bp      DNA      1linear      GSS 13-DEC-2000
LOCUS      1M0436G12P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0436G12 F, genomic survey sequence.
ACCESSION      AZ610868
VERSION      AZ610868.1 GI:11733058
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL      Contact: Robert B. Weiss
COMMENT      University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0436 row: G column: 12
            Seq primer: CCGTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0436G12"
                /sex="Male"
                /lab_host="R. Col1 strain XL10-Gold, T1-resistant, F-"
                /clone.lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: pMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to

```

adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5391 TTTAAAAATACAAAAA 5408
|||||
Db 19 TTTAAAAATACAAAAA 2

RESULT 603
A2627840 21 bp DNA linear GSS 13-DEC-2000
LOCUS A2627840.1
DEFINITION 1M0674D05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474B05 F, genomic survey sequence.

ACCESSION A2627840
VERSION A2627840.1 GI:11750126
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: B column: 05
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474B05"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5398 AATACAAAAAGAAAAA 5415
|||||
Db 21 AATACAAAAAGAAAAA 4

RESULT 604
A2764492 21 bp DNA linear GSS 16-FEB-2001
LOCUS A2764492
DEFINITION 1M0560D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560D04 R, genomic survey sequence.

ACCESSION A2764492
VERSION A2764492.1 GI:12879511
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: D column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560D04"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 TTTAAAAATTCACAAAAA 5408
|||||
3 TTTAAAAATTCACAAAAA 20

RESULT 605
CL693164

LOCUS PRI0160a_G09_2 - PRI0160a.BR (21) Mixed stage fosmid library of P.
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL693164
VERSION CL693164
KEYWORDS GI:50215072
SOURCE GSS.
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 21)

REFERENCE Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AUTHORS AppADB: an Acedb database for the nematode satellite organism
TITLE Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.bomme@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source Location/Qualifiers

1..21
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pGPfos-5 Fosmid vector"

Query Match 0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 TTTAAAAATTCACAAAAA 5410
|||||
4 TTTAAAAATTCACAAAAA 21

RESULT 606
CL693188

LOCUS PRI0160c_F06_2 - PRI0160c.BR (21) Note: Recurring string Mixed
DEFINITION stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL693188
VERSION CL693188
KEYWORDS GI:50215096
SOURCE GSS.
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 21)

AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an Acedb database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.bomme@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source Location/Qualifiers

1..21
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pGPfos-5 Fosmid vector"

Query Match 0.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 TTTAAAAATTCACAAAAA 5410
|||||
4 TTTAAAAATTCACAAAAA 21

RESULT 607
AZ363907 19 bp DNA linear GSS 02-OCT-2000
LOCUS IM0109113R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0109113 R, genomic survey sequence.
ACCESSION AZ363907
VERSION AZ363907
KEYWORDS GI:10477607
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,R., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: 1 column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0109113"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAA 5408
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 608
AA954509/c
LOCUS AA954509 19 bp mRNA linear EST 23-JUN-1998
DEFINITION on81d05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563081 3' similar to TR:Q24035 Q24035 ENA POLYPEPTIDE.
ACCESSION AA954509
VERSION AA954509.1 GI:3118204
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov
This clone is available royalty-free through LNL; contact the IMAS Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 754 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1563081"
/lab_host="PH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CCAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687339, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3762 GGGCCCCGAGGGCCTGNG 3780
Db 19 GGGGCCCGGGGCTGCG 1

RESULT 609
AJ666205/c
LOCUS AJ666205 19 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ666205 CSEORAN09 Sus scrofa cDNA clone C0000033_E15, mRNA sequence.
ACCESSION AJ666205
VERSION AJ666205.1 GI:49350656
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
1 (bases 1 to 19)
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross-match with the -minscore 20 and -mismatch 12 options. Vector:pBluescriptII(KS+). R. Site 1: EcoRI. R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..19
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_E15"
/tissue_type="Placenta"
/clone_lib="CSEORAN09"
/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5399 ATCAAAAAAAAAAATG 5417
Db 19 AAAAAAAAAAAGAAAAAAG 1

RESULT 610
AJ668179/c
LOCUS AJ668179 19 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ668179 CSEORAN09 Sus scrofa cDNA clone C0000045_L19, mRNA sequence.
ACCESSION AJ668179
VERSION AJ668179.1 GI:49352630
KEYWORDS EST.

SOURCE
ORGANISM
Sus scrofa (pig)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 19)
Anderson, S.I., Flinlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -mnscore 20 and -mismatch 12 options. Vector: pBluescriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.airgenomics.org.

FEATURES
source
1. 19
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000045.1.19"
/issue_type="placenta"
/clone_lib="CSEORAN09"
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAGAA 5411
|||||
19 AAAAAAAAAAAAAAAAAA 1

Db 19 AAAAAATACAAAAGAA 5411
|||||
19 AAAAAAAAAAAAAAAAAA 1

RESULT 611
AJ669138 19 bp mRNA linear EST 28-JUN-2004
LOCUS
DEFINITION
AJ669138 CSEORAN09 Sus scrofa cDNA clone C0000048_O12, mRNA
SEQUENCE
AJ669138
VERSION
KEYWORDS
SOURCE
EST.
Sus scrofa (pig)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 19)
Anderson, S.I., Flinlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -mnscore 20 and -mismatch 12 options. Vector: pBluescriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.airgenomics.org.

FEATURES
source
1. 19
/organism="Sus scrofa"
/mol_type="mRNA"

/db_xref="taxon:9823"
/clone="C0000048_O12"
/issue_type="placenta"
/clone_lib="CSEORAN09"
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAGAA 5411
|||||
19 AAAAAAAAAAAAAAAAAA 1

Db 19 AAAAAATACAAAAGAA 5411
|||||
19 AAAAAAAAAAAAAAAAAA 1

RESULT 612
BQ588729 19 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
BQ588729 5013713-024-014-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris cDNA clone 024-014-B24 3-PRIME, mRNA sequence.
ACCESSION
BQ588729
VERSION
KEYWORDS
SOURCE
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 19)
Herwig, R., Schulz, B., Welschhaer, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehnach, H. and Radeloff, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED
122362189
12472698
CONTACT: Welschhaer B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: welschhaer@mpiz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 14 row: B column: 24
Seq primer: T7; GTAATACGACCTCCTCATATAGGC.
location/Qualifiers
1. 19
/organism="Beta vulgaris"
/mol_type="mRNA"
/culturvar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:187281"
/db_xref="taxon:161934"
/clone="024-014-B24"
/issue_type="storage root"
/lab_host="EMD110B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet. Library provided by KWS Kleinfanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

	Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	5393	AAAAAAAAATCACAAAAAGAA	5411							
Db	1	AAAAAAAAAAAAAAAAAAAAA	19							

RESULT 613				
CB174047/C				
LOCUS	CB174047	19 bp	mRNA	linear EST 09-OCT-2003
DEFINITION	OR 2032F05 010529.y1 Adult mouse olfactory epithelium library Mus musculus cDNA clone 2032F05 5', mRNA sequence.			

ACCESSION	CB174047
VERSION	CB174047.1
KEYWORDS	GI:37592676
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE
AUTHORS

Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priiddy, L., Ross, J.A.,
1 (bases 1 to 19)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE	Olfactory receptor expressed sequence tags
JOURNAL	expression of over 400 genes, extensive
COMMENT	unequal expression levels
	Genome Biol. 4 (11), R71.1-R71.15 (2003)
	Contact: Young JM

Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98109-1024, USA
tel: 206 616 1471

Source	1-19
Features	Location/Qualifiers
	Seq primer: M13 Reverse.
	Email: jayoung@hrc.org

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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2032P05"
/rnause_type="Olfactory and respiratory epithelium"
/dev_stage="Adult"
/clone_id="Adult mouse olfactory epithelium library"
/notes="Organ: Olfactory tubercles; Vector:
lambdaZAPRI-X; Site 1: EcoRI; Site 2: XhoI. This library
was provided by Leslie Vosshall. mRNA was prepared from
the olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPRI-XR vector."

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Query Match	0.3%	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%	Pred. No. 4e+02;		
Matches	16;	Conservative	0;	Mismatches 3;
			Indels	0;
			Gaps	0

QY	5393	AAAAAAAAATACAAAAAGAA	5411
Db	19	AAAAAAAAAAAAAAAAAAAA	1

RESULT 614	CF279008/c	LOCUS	DEFINITION
	CF279008	19 bp mRNA	EST 14-AUG-2001
	14ETL--05-C13.b1	Rice etiolated leaf	plasmid cDNA library (14ETL)
	Oryza sativa (japonica cultivar-group)	CDNA clone	14ETL--05-C13,
	mRNA sequence		

Accession	GI
CF279008	33656394
CF279008.1	33656394

KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Equisetidae; Streptophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Enarthroidae; Oryzae; Oryza.				
1 (pages 1 to 19)				
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. K. and Nahn, B. H.				
Large-scale Sequencing Analysis of Rice ESTs				
Unpublished (2003)				
Contact: Nahn B. H.				

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:3947"
/clone="14RTL-05-C13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14RTL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI, mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match	0.3%	Score 14.2;	DB 1;	length 19;
Best Local Similarity	84.2%;	Pred. No. 4e+02;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 5393 AAAAAAAAAACAAAGAGAA 5411
||||| | ||||| ||
DQ 19 AAAAAAAAAAAAAAAAAA 1

RESULT 615	CF291089/c	LOCUS	DEFINITION
	CF291089	19 bp	RNA linear EST 14-AUG-2000
	14RCOT-01-G03.b1	Rice root plasmid cDNA library (14RCOT)	Oryza sativa [Japanica cultivar-group] cDNA clone 14RCOT-01-G03, mRNA sequence.

ACCESSION	CP291089
VERSION	CP291089.1
KEYWORDS	GI:33660122
SOURCE	EST.
	<i>Oryza sativa</i> (japonica cultivar-group)

ORGANISM
Oryza sativa (Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; *Oryza*.
1 (base) 1 50 10

REFERENCES	Kim, Y.C., Lee, T.H., Shin, Y.C., Kim, U.S., Jun, K.M., Cheong, P.J., Kim, M.J., Song, S.I., Kim, J.K., Kim, Y.K., and Nam, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nam B.H.
AUTHORS	Kim, Y.C., Lee, T.H., Shin, Y.C., Kim, U.S., Jun, K.M., Cheong, P.J., Kim, M.J., Song, S.I., Kim, J.K., Kim, Y.K., and Nam, B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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"source": "Jorgensen-Oryza sativa (japonica cultivar-group)",
"mol_type": "mrna",
"cultivar": "nakhdong",
"db_xref": "taxon:39847",
"clone": "14K01-01",
"tissue_type": "root",
"dev_stage": "14 days after germination"

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/lab host="E.coli DH10B"
/clone lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAGAA 5411
|||||
19 AAAAAAAAAAAAAAAAAA 1

RESULT 616
CF291090 19 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-G03.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA
sequence.
ACCESSION CF291090.1 GI:33660123
VERSION CF291090
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-G03"
/issue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAGAA 5411
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19 AAAAAAAAAAAAAAAAAA 19

RESULT 617
CF298396/c 19 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M05, mRNA
sequence.
ACCESSION CF298396
VERSION CF298396.1 GI:33670157

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="7LEAF--01-M05"
/issue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5402 CAAAAGAAAAGAA 5420
|||||
19 CAAAAAAAAAAAAAAAAA 1

RESULT 618
CF298472/c 19 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--01-001.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-001, mRNA
sequence.
ACCESSION CF298472
VERSION CF298472.1 GI:33670233
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db xref="taxon:39947"
/c1one="7LEAF--01-C01"
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/dev stage="7 days after germination"
/lab host="E.coli DH10B"
/clone.lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes=vector: pCR4-TOPO, site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5397 AATTCAGAAAAAGAAAAA 5415
      ||||| ||||| |||||
      19 ATATGAAAAAAAAAAAAAAAAA 1

RESULT 619
LOCUS CF299598/c
DEFINITION CF299598 19 bp mRNA linear EST 15-AUG-2003
sativa (japonica cultivar-group) cDNA library II (7LEAF) Oryza
sequence.
ACCESSION CF299598.1 GI:33671359
VERSION CF299598.1
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
          1 (bases 1 to 19)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc., Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Gyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
      source
      1..19
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="7LEAF--03-K23"
      /tissue_type="leaf"
      /dev stage="7 days after germination"
      /lab_host="E.coli DH10B"
      /clone.lib="Rice leaf plasmid cDNA library II (7LEAF)"
      /note=vector: pCR4-TOPO, site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."

RESULT 620
LOCUS CF300236/c
DEFINITION CF300236 19 bp mRNA linear EST 15-AUG-2003
sativa (japonica cultivar-group) cDNA library II (7LEAF) Oryza
sequence.
ACCESSION CF300236.1 GI:33671359
VERSION CF300236.1
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
          1 (bases 1 to 19)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc., Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Gyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
      source
      1..19
      /organism="Oryza sativa (japonica cultivar-group)"
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      /tissue_type="leaf"
      /dev stage="7 days after germination"
      /lab_host="E.coli DH10B"
      /clone.lib="Rice leaf plasmid cDNA library II (7LEAF)"
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      with oligoribonucleotides and then used as templates for
      RT-PCR."

Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAAGAA 5411
      ||||| ||||| |||||
      19 AAAAAAAAAAAAAAAAAA 1

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ACCESSION	CF300236	sativa [japonica cultivar-group]	cDNA clone 7LEAF--04-124, mRNA sequence.
VERSION	CF300236.1	GI:33671997	
KEYWORDS	EST.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	Oryza sativa (japonica cultivar-group)		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Eubartoideae; Oryzaceae; Oryza.		
TITLE	1 (bases 1 to 19)		
JOURNAL	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.		
COMMENT	Large-scale Sequencing Analyses of Rice ESTs Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.		
FEATURES	location/Qualifiers		
source	1..19		
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	/mol_type="mRNA"		
	/cultiVar="Nackdong"		
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	/issue_type="leaf"		
	/dev_stage="7 days after germination"		
	/lab_host="E.coli DH10B"		
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	/note="Vector: PCR4-TOPo; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."		
Query Match	0.3%; Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%;	Pred. No. 4e+02;	
Matches	16;	Conservative 0;	Mismatches 3;
		Indels 0;	Gaps 0;
Dn	5389 AATTAAAAAATACAAA 5407		
	19 AATCAAAAAAAAAAAAA 1		
RESULT 621			
CP302327	19 bp	mRNA	linear
LOCUS	7LEAF--07-L24.b1	Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group)	cDNA clone 7LEAF--07-L24, mRNA sequence.
DEFINITION	Sequence.		
ACCESSION	CF302327		
VERSION	CF302327.1	GI:33674088	
KEYWORDS	EST.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Eubartoideae; Oryzaceae; Oryza.		
AUTHORS	1 (bases 1 to 19)		
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.		
JOURNAL	Large-scale Sequencing Analyses of Rice ESTs		
COMMENT	Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.		
FEATURES	location/Qualifiers		

source

1.19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="rRNA"

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/db_xref="taxon:39947"

/clone="7LEAF--07-L24"

/issue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 4e+02; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3;

Oy 5393 AAAAAAAAAATCAAAAAAGA 5411

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 622

CF302456/c 19 bp mRNA linear EST 15-AUG-2003

LOCUS 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P22, mRNA

sequence.

ACCESSION

CF302456

CF302456.1 GI:33674217

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of BioScience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1.19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="rRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--07-P22"

/issue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5402 AAAAAAAAAATCAAAAAAGA 5420

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 623

CF304589/c 19 bp mRNA linear EST 15-AUG-2003

LOCUS ABP1--05-G10.g1 ABP3-overexpressing transgenic rice lambda phage

DEFINITION cDNA library (ABP1) Oryza sativa (japonica cultivar-group) cDNA

clone ABP1--05-G10, mRNA sequence.

ACCESSION

CF304589

CF304589.1 GI:33676350

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

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Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1.19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="rRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABP1--05-G10"

/issue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="ABP3-overexpressing transgenic rice lambda

phage cDNA library (ABP1)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was dried for 2hrs. cDNA was inserted into

lambda uni-ZAP XR vector at 5' end with EcoRI and 3' end

with XhoI site. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 4e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAATCAAAAAAGA 5411

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 624

CF309636/c 19 bp mRNA linear EST 15-AUG-2003

LOCUS ABP--03-008.g1 ABP3-overexpressing transgenic rice plasmid cDNA

DEFINITION library (ABP) Oryza sativa (japonica cultivar-group) cDNA clone

ABP--03-008, mRNA sequence.

ACCESSION

CF309636

CF309636.1 GI:33681397

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

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1..19
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
CDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5390 ATTTAAAAATACAAAAA 5408
|||||
19 ATTCAAAAAA 1

RESULT 625

CF309801/c

LOCUS

ABF--04-C04.g1 ABF3-overexpressing transgenic rice plasmid CDNA
library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone
ABF--04-C04, mRNA sequence.

ACCESSION

CF309801

VERSION

EST.

KEYWORDS

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzae; Oryza.

REFERENCE

1 (bases 1 to 19)

Klim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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CDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried

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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5411
|||||
19 AAAAAA 1

RESULT 626

CF309943

LOCUS

ABF--04-F15.b1 ABF3-overexpressing transgenic rice plasmid CDNA
library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone
ABF--04-F15, mRNA sequence.

ACCESSION

CF309943

VERSION

EST.

KEYWORDS

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzae; Oryza.

1 (bases 1 to 19)

Klim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
CDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAAGAA 5411
|||||
19 AAAAAA 1

RESULT 627

CF311496

LOCUS

ABF--06-L18.g1 ABF3-overexpressing transgenic rice plasmid CDNA
library (ABF) Oryza sativa (japonica cultivar-group) CDNA clone
ABF--06-L18, mRNA sequence.

ACCESSION CF311496
VERSION CF311496.1 GI:33683257
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group); Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid CDNA library (ABF)"
/note="Vector: pCR4-TOPO, site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATGCAGAAAAAGAA 5411
|||||
19 AAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 629
CF311513 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-M03, mRNA sequence.
ACCESSION CF311513
VERSION CF311513.1 GI:33683274
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group); Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid CDNA library (ABF)"
/note="Vector: pCR4-TOPO, site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATGCAGAAAAAGAA 5411
|||||
19 AAAAAAAAAAAAAAAAAAAAAA 1

Db

RESULT 629
CF312403 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-C07.b1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-C07, mRNA sequence.
ACCESSION CF312403
VERSION CF312403.1 GI:33684164
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group); Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

/cissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="R.coli DH10B"
/clone_11b="OshDACL-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAAGAA 5411
|||||
1 AAAAAAAAAAAAAAAAAA 19

RESULT 633
CF329136/c 19 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA
sequence.

ACCESSION CF329136 GI:33806509
VERSION CF329136
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..19
location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiVar="Nackdong"
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/lab_host="R.coli DH10B"
/clone_11b="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5397 AAAAAATACAAAAAGAA 5415
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19 AAAAAAAAAAAAAAAAAA 1

RESULT 634
CF329137 19 bp mRNA linear EST 18-AUG-2003
LOCUS CF329137

DEFINITION NACL--04-F15.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA
sequence.

ACCESSION CF329137 GI:33806511
VERSION CF329137
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..19
location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiVar="Nackdong"
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/cissue_type="callus"
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/lab_host="R.coli DH10B"
/clone_11b="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5395 AAAAAATACAAAAAGAA 5413
|||||
1 AAAAAATACAAAAAGAA 19

RESULT 635
CF329986 19 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--05-109.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-109, mRNA
sequence.

ACCESSION CF329986 GI:33808194
VERSION CF329986
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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RESULT 636
CF329987 19 bp mRNA linear EST 18-AUG-2003
LOCUS CF329987

Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers

1. 19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-M08"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="AtUMT-overexpressing transgenic rice plasmid
CDNA library (UMT)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
1 AAAAAAAAAAAAAAAAAA 19

Db

RESULT 639
CF334014/C 19 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--03-C09.G1 AtUMT-overexpressing transgenic rice plasmid CDNA
DEFINITION library (UMT) Oryza sativa (japonica cultivar-group) CDNA clone
JMT--03-C09, mRNA sequence.
ACCESSION CF334014.1 GI:33816333
VERSION CF334014.1
KEYWORDS Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers

1. 19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--03-C09"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="AtUMT-overexpressing transgenic rice plasmid
CDNA library (UMT)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
19 AAAAAAAAAAAAAAAAAA 1

Db

RESULT 640
CN545602/C 19 bp mRNA linear EST 30-APR-2004
LOCUS EST17546 Ripe Grape Skin Triplex2 library Vitis vinifera cDNA
DEFINITION clone B3CS00RL003H10 3', mRNA sequence.
ACCESSION CN545602.1 GI:46910227
VERSION CN545602
KEYWORDS EST.
SOURCES Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 19)
AUTHORS Abbal,P., Agase,A., Agorger,A., Aranasova,R., Barrieu,F.,
Couture,C., Dedaidechamp,F., Delrot,S., Gillesse,D., Grimplet,J.,
Hamdi,S., Komieu,C. and Terrier,N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.

FEATURES
source
Location/Qualifiers

1. 19
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/dev_stage="ripening stage"
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/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
5'11a; Site_2: 5'11b; Oriented library"

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
19 AAAAAAAAAAAAAAAAAA 1

Db

RESULT 641
CN545922/C 19 bp mRNA linear EST 30-APR-2004
LOCUS EST 17866 Ripe Grape Skin Triplex2 library Vitis vinifera cDNA
DEFINITION clone B3CS00RL006D07 3', mRNA sequence.
ACCESSION CN545922.1 GI:46910547
VERSION CN545922
KEYWORDS EST.
SOURCES Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosidae; Vitaceae; Vitis.
1 (bases 1 to 19)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Gissant,D., Grimplet,J.,
Hamdi,S., Romeu,C. and Terrier,N.
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or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
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France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..19
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D07"
/dev_stage="ripening stage"
/clone.lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. NO. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAATTCAAAAGAA 5411
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 642
LOCUS CNE45964 19 bp mRNA EST 30-APR-2004
DEFINITION EST 17912 Ripe Grape Skin Triplex2 Library Vitis vinifera CDNA
clone B3CS00RL006H10 3', mRNA sequence.
ACCESSION CNE45964
VERSION CNE45964.1 GI:46910589
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Vitis vinifera
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosidae; Vitaceae; Vitis.
1 (bases 1 to 19)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Gissant,D., Grimplet,J.,
Hamdi,S., Romeu,C. and Terrier,N.
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or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
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Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..19
/organism="Vitis vinifera"
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/cultivar="Cabernet Sauvignon"
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/clone.lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
SOURCE
Location/Qualifiers
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/cultivar="Cabernet Sauvignon"
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/dev_stage="ripening stage"
/clone.lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
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/mol_type="mRNA"
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/db_xref="taxon:29760"
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/dev_stage="ripening stage"
/clone.lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
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Location/Qualifiers
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/db_xref="taxon:29760"
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/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
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Location/Qualifiers
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/dev_stage="ripening stage"
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/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
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FEATURES
SOURCE
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D07"
/dev_stage="ripening stage"
/clone.lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
SOURCE
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
SOURCE
Location/Qualifiers
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/cultivar="Cabernet Sauvignon"
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/dev_stage="ripening stage"
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sf1A; site_2: sf1B; Oriented library"

FEATURES
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FEATURES
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Location/Qualifiers
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FEATURES
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Location/Qualifiers
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FEATURES
SOURCE
Location/Qualifiers
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sf1A; site_2: sf1B; Oriented library"

FEATURES
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Location/Qualifiers
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FEATURES
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FEATURES
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FEATURES
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/dev_stage="ripening stage"
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/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
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FEATURES
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FEATURES
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/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
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Location/Qualifiers
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/clone.lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
SOURCE
Location/Qualifiers
1..19
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sf1A; site_2: sf1B; Oriented library"

FEATURES
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Location/Qualifiers
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sf1A; site_2: sf1B; Oriented library"

FEATURES
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/db_xref="taxon:29760"
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/clone.lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: lambda Triplex2; site_1:
sf1A; site_2: sf1B; Oriented library"

FEATURES
SOURCE
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Cab
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Query Match          0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      5393 AAAAAAAAAACAAAAGAA 5411
         ||||| | ||||| ||
Db       19 AAAAAAAAAAAAAAAAAA 1

RESULT 643
LOCUS    CN546303/c
DEFINITION EST 30-APR-2004
            CDS     19 bp mRNA linear
ACCESSION CN546303
VERSION   CN546303
KEYWORDS  EST.
SOURCE    Vitis vinifera
ORGANISM  Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; Vitaceae; Vitis.
           1 (bases 1 to 19)
           Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
           Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
           Hamdi,S., Romieu,C. and Terrier,L.
           Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
           or seeds) at Various Developmental Stages
           Unpublished (2002)
JOURNAL   Contact: Hamdi S.
COMMENT   UMR 619 - Equipe Biologie de la Vigne
           Universite de Bordeaux I, Institut National de la Recherche
           Agronomique
           71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
           France
           Tel.: 00-33-(0)5-57-12-25-50
           Fax: 00-33-(0)5-57-12-25-48
           Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Vitis vinifera"
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                     /cldn="B3CSIXGB015E10"
                     /dev_stage="green stage"
                     /clone_1lb="Green Grape Berry Lambda Triplex2 Library"
                     /note="Organ: Fruit without seeds; Vector: Lambda
                     Triplex2; Site_1: SfIIA; Site_2: SfiIB; Oriented library"

Query Match          0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      5393 AAAAAAAAAACAAAAGAA 5411
         ||||| | ||||| ||
Db       19 AAAAAAAAAAAAAAAAAA 1

RESULT 644
LOCUS    AZ307313
DEFINITION IM0008H2OR Mouse 10kb plamid U0GCIM library Mus musculus genomic

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ACCESSION	clone UGCG1M0008H20 R, genomic survey sequence.
VERSION	AZ307313
KEYWORDS	AZ307313.1 GI:10346192
SOURCE	GS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Baccorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center University of Utah Rm. 3102, Bldg 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0008 row: H column: 20 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence atop: 19. Location/Qualifiers 1..19
FEATURES	
source	

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Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393  AAAAAAAAAATCAAAAAAAAAAGAA 5411
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Db       1  AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 645
LOCUS      AZ310079/c
DEFINITION AZ310079 19 bp DNA linear GSS 29-SEP-2000
            1M001817 R, genomic survey sequence.
            Clone UUGC1M001817 R, genomic survey sequence.

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ACCESSION	AZ310079
VERSION	AZ310079.1
KEYWORDS	GI:10351709
SOURCE	GS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
TITLE	1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Petersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright D.Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0018 row: K column: 17 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1. .19
FEATURES	
SOURCE	

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Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Prod. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393  AAAAAAAAAACAAAAAGAA 5411
          ||||| | ||||| |
Db       19  AAAAAAAAAAAAAAAAAAAAA 1

RESULT 646
AZ310105/c      19 bp      DNA      linear      GSS 29-SEP-2000
LOCUS          AZ310105
DEFINITION      IM0018B21R Mouse 10kb plasmid UNGC1M library Mus musculus genomic
ACCESSION      clone UNGC1M0018B21 R, genomic survey sequence.
                AZ310105

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VERSION      AZ310105.1  GI:10351761
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
              1 (bases 1 to 19)
              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
              Irlam, H., Longacre, S., Mahmond, M., Meenen, E., Pedersen, T.,
              Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
              Niederhausern, A. and Wright, D., Weis, R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL      Contact: Robert B. Weis
COMMENT      University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84102, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunne@genetics.utah.edu
              Insert Length: 10000   Std Error: 0.00
              Plate: 0018   row: B   column: 21
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 19.
              Location/Qualifiers
              1..19
  
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 "/mol_type="genomic DNA"
 "/strain="C57BL/6J"
 "/db_xref="taxon:10090"
 "/clone="UUCGM0018B21"
 "/sex="Male"
 "/lab_host="E. Coli strain XL10-Gold, T4-resistant, F-"
 "/clone_1lb="Mouse 10kb plasmid UUCGM library"
 "/note="Vector: PMD42n; Purified genomic DNA from M.
 "musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 [g1473214|gb|AF12972.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.3%;	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%;	Pred. No. 4e+02;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0

QY	5393	AAAAAAAAATACAAAAAGAA	5411
Dd	19	AAAAAAAAAAAAAAAAAAAAA	1

RESULT	647
AZ317743	
LOCUS	AZ317743
DEFINITION	19 bp DNA linear GSS-29-sep-2000
ACCESSION	IM0036618 Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0036618 R, genomic survey sequence.
VERSION	AZ317743
	GI:10366848
	AZ317743.1

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eumayorita; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0036 Row: B Column: 18
Seq primer: CACACAGAAAACAGCTTAGCC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

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/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"  

/clone_1ib="Mouse 10kb plasmid UGGCM library"  

/note="Vector: PMD42ny; Purified genomic DNA from M.  

musculus C57BL/6J (male) was obtained from the Jackson  

Laboratory Mouse DNA Resource  

(http://www.jax.org/resources/documents/dnares/). The DNA  

was hydrodynamically sheared by repeated passage through a  

0.005 inch orifice at constant velocity. The sheared DNA  

was blunt end-prepared with T4 DNA polymerase and T4  

polynucleotide kinase. Adaptor oligonucleotides were  

ligated to the blunt ends in high molar excess. The  

adaptor DNA was purified and size-selected for a 9.5 to  

10.5 kb range using preparative agarose gel  

electrophoresis. Vector DNA was prepared from a derivative  

of PMD42 [g14732114.9b]/AF12072.1), a copy-number  

inducible derivative of plasmid R1. The vector was ligated  

with adaptors complementary to the insert adaptors and  

purified. The sheared, adaptor mouse DNA was annealed to  

adaptor vector DNA, and transformed into  

chemically-competent E. coli XL10-Gold (Stratagene) cells  

and selected for ampicillin resistance."

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Query Match	0.3%	Score 14.2;	DB 1;	Length 19;
Best Local Similarity	84.2%;	Pred. No. 4e+02;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

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Db      1 AAAAAAAAAAAAAAAAAAAAAA 19
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RESULT	648
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ACCESSION	AZ340311
VERSION	AZ340311.1 GI:10415441
KEYWORDS	GSS.

ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tunney, A., von Niederhausen, A. and Wright, D., Weis, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center
COMMENT	Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0080 row: F column: 06 Seq primer: CGGTGTAAACGACGCACAT Class: plasmid High quality sequence stop: 19. Location/Qualifiers 1..19 /organism="Mus musculus"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/note="Vector: PWD22N; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD22 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.3%	Score 14.2	DB 1	Length 19
Best Local Similarity	84.2%	Pred. No. 4e+02		
Matches	16	Conservative	0	Mismatches 3
				Indels 0
				Gaps 0
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DEFINITION	IM0088A10F Mouse 10kb plasmid. tUGC1M library Mus musculus genomic			
ACCESSION	AZ350519			
VERSION	AZ350519.1	GI:10429756		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: A column: 10
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Class: plasmid ends
High quality sequence stop: 19.
location/Qualifiers
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAA 5411
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 651
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DEFINITION IM0110524F Mouse 10kb plasmid UUCGCM library Mus musculus genomic clone UUCGCM0110524 F, genomic survey sequence.
ACCESSION AZ364226
VERSION AZ364226.1 GI:10477926
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 19.
location/Qualifiers
1..19
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/clone_lib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAAGAA 5411
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 652
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DEFINITION IM0112A07R Mouse 10kb plasmid UUCGCM library Mus musculus genomic clone UUCGCM0112A07 R, genomic survey sequence.
ACCESSION AZ365696
VERSION AZ365696.1 GI:10479396
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islem,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0112 row: A column: 07
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
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 /db_xref="taxon:10090"
 /clone="UUCG1M0112A07"
 /sex="Male"
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 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAACAAAAAGAA 5411
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RESULT 653
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 ACCESSION AZ374409
 VERSION AZ374409.1 GI:10488109
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islem,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0127 row: D column: 10
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /clone_1lb="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAACAAAAAGAA 5411
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RESULT 654
 LOCUS AZ374619 19 bp DNA linear GSS 02-OCT-2000
 DEFINITION IM0127F04R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 clone UUCG1M0127F04 R, genomic survey sequence.
 ACCESSION AZ374619
 VERSION AZ374619.1 GI:10488119
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: F column: 04
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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/clone_11b="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gbl|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 655
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DEFINITION 1M014410R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M014410 R, genomic survey sequence.
ACCESSION AZ385952
VERSION AZ385952.1 GI:10499652
KEYWORDS GSS.

SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0144 row: L column: 10
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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/clone_11b="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gbl|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 656
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DEFINITION 1M0153K08R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0153K08 R, genomic survey sequence.
ACCESSION AZ391509
VERSION AZ391509.1 GI:10506552
KEYWORDS GSS.

SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0153 row: K column: 08
Seq primer: CACACAGGAAACAGCTATAC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
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/clone_1lb="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
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of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411
|||||
1 AAAAAAAAAAAAAAAAAA 19

RESULT 657
AZ410050
LOCUS AZ410050 19 bp DNA linear GSS 03-OCT-2000
DEFINITION IM018204F Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM018204 F, genomic survey sequence.
ACCESSION AZ410050
VERSION AZ410050.1 GI:10534063
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: P column: 04
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0182P04"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent B. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411
|||||
1 AAAAAAAAAAAAAAAAAA 19

RESULT 658
AZ414413
LOCUS AZ414413 19 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0188013R Mouse 10kb plasmid UUCGM library Mus musculus genomic
clone UUCGM0188013 R, genomic survey sequence.
ACCESSION AZ414413
VERSION AZ414413.1 GI:10538426
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, R., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0188 row: 0 column: 13
Seq primer: CACACAGAAACAGCTATCACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No.4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
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1 AAAAAAAAAAAAAAAAAA 19

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 659
A2422604 19 bp DNA linear GSS 03-OCT-2000
LOCUS A2422604
DEFINITION 1M0201B21F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0201B21 F, genomic survey sequence.
ACCESSION A2422604
VERSION A2422604.1 GI:10546617
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: B column: 21
Seq primer: CATTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0201B21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No.4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
|||||
1 AAAAAAAAAAAAAAAAAA 19

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 660
A2424716 19 bp DNA linear GSS 03-OCT-2000
LOCUS A2424716
DEFINITION 1M0204O20F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0204O20 F, genomic survey sequence.
ACCESSION A2424716
VERSION A2424716.1 GI:10546729
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0204 row: 0 column: 20
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

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1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0204020"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 661

A2441329/c

LOCUS

DEFINITION 1M0233D01F Mouse 10kb plasmid UUCG1M library Mus musculus genomic

ACCESSION

A2441329

VERSION

A2441329.1 GI:10565342

KEYWORDS

SOURCE

ORGANISM

MUS musculus (house mouse)

Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

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University of Utah

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0233 row: 0 column: 01

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUCG1M0233D01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 662

A2442365/c

LOCUS

DEFINITION 1M0236C13F Mouse 10kb plasmid UUCG1M library Mus musculus genomic

ACCESSION

A2442365

VERSION

A2442365.1 GI:10565378

KEYWORDS

SOURCE

ORGANISM

MUS musculus (house mouse)

Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

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 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0266 Row: B Column: 03
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0265B03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAACAAAAGAA 5411
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 665
 AZ471494/c 19 bp DNA linear GSS 04-OCT-2000
 LOCUS IM0286E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0286E11 F, genomic survey sequence.
 ACCESSION AZ471494
 VERSION AZ471494.1 GI:10629619
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 JOURNAL University of Utah Genome Center
 COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0286 Row: B Column: 11
 Seq primer: CCGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

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 /strain="C57BL/6J"
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 /clone="UUGC1M0265E11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5393 AAAAAAAAAACAAAAGAA 5411
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 666
 AZ476576/c 19 bp DNA linear GSS 04-OCT-2000
 LOCUS IM0295F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0295F04 R, genomic survey sequence.
 ACCESSION AZ476576
 VERSION AZ476576.1 GI:10634701
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 JOURNAL University of Utah Genome Center
 COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 04
Seq primer: CACACAGGAAACGCTATACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1..19
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0315D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAA 5411
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 667
LOCUS AZ486786 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0315D21F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0315D21 F, genomic survey sequence.
ACCESSION AZ486786
VERSION AZ486786.1 GI:10653902
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: D column: 21
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1..19
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0315D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATCAAAAAGAA 5411
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 668
LOCUS AZ490652 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0323B17R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0323B17 R, genomic survey sequence.
ACCESSION AZ490652
VERSION AZ490652.1 GI:10661595
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0323 row: E column: 17
 Seq primer: CACACAGCAACGCTATACG
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0323817"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
 Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 669
 AZ508040 19 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0350804F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0350804 F, genomic survey sequence.
 ACCESSION AZ508040
 VERSION AZ508040.1 GI:10689356
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0350 row: B column: 04
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

1. 19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0350804"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
 Best Local Similarity 84.2%; Pred. No. 4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 670
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 LOCUS 1M0354A07F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0354A07 F, genomic survey sequence.
 ACCESSION AZ509929
 VERSION AZ509929.1 GI:10691245
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0354 row: A column: 07

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

1..19

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0354A07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5401 ACAAAGAAAGAAATGAA 5419
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 671

AZ579119 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0363M16F Mouse 10kb plasmid U08C1M library Mus musculus genomic

DEFINITION Clone U08C1M0363M16 F, genomic survey sequence.
ACCESSION AZ579119
VERSION AZ579119.1 GI:11693580
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Istam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: M column: 16

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="U08C1M0363M16"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAGAA 5411
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 672

AZ583970 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0388M1F Mouse 10kb plasmid U08C1M library Mus musculus genomic

DEFINITION Clone U08C1M0388M1 F, genomic survey sequence.
ACCESSION AZ583970
VERSION AZ583970.1 GI:11704386
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Istam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0388 row: M column: 11

Seq primer: CGTGTAAACGACGCCAGT

FEATURES High quality sequence stop: 19.

source Location/Qualifiers

1.19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0391D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAGAA 5411
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Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 673
AZ585865 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0391D21F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION Clone UUC1M0391D21 F, genomic survey sequence.
ACCESSION AZ585865
VERSION AZ585865.1 GI:11708055
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,B.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: D column: 21
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES source

Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0391D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAGAA 5411
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 674
AZ593210 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0404C09R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION Clone UUC1M0404C09 R, genomic survey sequence.
ACCESSION AZ593210
VERSION AZ593210.1 GI:11715400
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,B.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0404 row: C column: 09
Seq primer: CACACGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

source

1. .19

/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0404C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gblAF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAAGAA 5411
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Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 675
A2616154/C 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0445P16R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0445P16 R, genomic survey sequence.
ACCESSION A2616154
VERSION A2616154.1 GI:11738344
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0445 row: P column: 16
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

FEATURES
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0445P16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gblAF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.3%; Score 14.2; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAAGAA 5411
||||| | ||||| |
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 676
A2627844/C 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0474J05F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0474J05 F, genomic survey sequence.
ACCESSION A2627844
VERSION A2627844.1 GI:11750130
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: J column: 05
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

FEATURES
source

/organism="Mus musculus"

/mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0486E01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 677

A2631701

LOCUS 19 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0486E01F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0486E01 F, genomic survey sequence.

ACCESSION A2631701

VERSION A2631701.1 GI:11753891

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel.: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0486 row: B column: 01

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0486E01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 4e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAAGAA 5411
 Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 678

A2633821

LOCUS 19 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0489H15F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0489H15 F, genomic survey sequence.

ACCESSION A2633821

VERSION A2633821.1 GI:11756011

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel.: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0489 row: H column: 15

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

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/mol_type="genomic DNA"

/strain="C57BL/6J"

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/db_xref="taxon:10090"
/clone="UUGC1M0489H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAGAA 5411
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 679
AZ643659 19 bp DNA linear GSS 14-DEC-2000
LOCUS IM0507D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0507D18 F, genomic survey sequence.
ACCESSION AZ643659
VERSION A2643659.1 GI:11771446
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0507 row: D column: 18
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="UUGC1M0507D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAGAA 5411
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 680
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LOCUS IM0508E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0508E17 R, genomic survey sequence.
ACCESSION AZ644698
VERSION A2644698.1 GI:11773485
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0508 row: E column: 17
Seq primer: CACACAGAAACGACTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0508E17"

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: pMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAATACAAAAAGAA 5411
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Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 681
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LOCUS 1M0511G04R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0511G04 R, genomic survey sequence.
ACCESSION AZ645841
VERSION AZ645841.1 GI:11775726
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: G column: 04
Seq primer: CACACAGAAACAGCATATACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
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/clone="UUC1M0511G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: pMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5407 AAGAAAAATGAAATTA 5425
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Db 19 AAAAAAAAAAGAAAAAAAAA 1

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RESULT 682
AZ648335 19 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0517L16F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0517L16 F, genomic survey sequence.
ACCESSION AZ648335
VERSION AZ648335.1 GI:11780699
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0517 row: L column: 16
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Class: plasmid ends
High quality sequence stop: 19.
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FEATURES
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/clone="UUC1M0511G04"
/sex="Male"
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
DB 1 AAAAAAAAAAAAAAAAAA 19

RESULT 683

LOCUS

A2649888 19 bp DNA linear GSS 14-DEC-2000

DEFINITION

IM0519E1SR Mouse 10kb plasmid UUC1M library Mus musculus genomic

ACCESSION

A2649888

VERSION

A2649888.1

KEYWORDS

GSS.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .19
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAACAAAGAA 5411
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 684

LOCUS

A2764497 19 bp DNA linear GSS 16-FEB-2001

DEFINITION

IM0560H03R Mouse 10kb plasmid UUC1M library Mus musculus genomic

ACCESSION

A2764497

VERSION

A2764497.1

KEYWORDS

GSS.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .19
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0560H03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/nares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAGAA 5411
DB 1 AAAAAAAAAAAAAAAAAA 19

RESULT 685
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LOCUS 1M0560E16R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION
A2764522
ACCESSION
A2764522.1 GI:12879571
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: E column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0560E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/nares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAGAA 5411
DB 1 AAAAAAAAAAAAAAAAAA 19

RESULT 686
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LOCUS 1M0560P14R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION
A2764534
ACCESSION
A2764534.1 GI:12879595
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: P column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Location/Qualifiers

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAA 5411
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 687
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LOCUS 1M0571L23R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0571L23 R, genomic survey sequence.
ACCESSION A2770387
VERSION A2770387.1 GI:12891520
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: L column: 23
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAGAA 5411
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 688
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LOCUS 2M008E01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCG2M008E01 R, genomic survey sequence.
ACCESSION A2775624
VERSION A2775624.1 GI:12902356
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weiss,R.
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JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5397 AATTCACCAAAAGCAAAA 5415
Db 1 ACACACCAAAAGCAAAA 19

RESULT 689
AZ778858 19 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M0014020F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCG2M0014020 F, genomic survey sequence.
ACCESSION
VERSION A2778858
KEYWORDS A2778858.1 GI:12908925
GSS.

SOURCE
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: 0 column: 20
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

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/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAATACCAAAAGCA 5411
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 690
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LOCUS
DEFINITION 2M001616F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCG2M001616 R, genomic survey sequence.
ACCESSION
VERSION A2779901
KEYWORDS A2779901.1 GI:12911024
GSS.

SOURCE
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: E column: 16
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Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

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/note="Vector: pMD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5393 AAAAAATACAAAAAGAA 5411
1 AAAAAAAAAAAAAAAAAA 19
Db

RESULT 691 19 bp DNA linear GSS 16-FEB-2001
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LOCUS 2M0021003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0021003 R, genomic survey sequence.
ACCESSION AZ781876
VERSION AZ781876.1 GI:12915007
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH GENOME CENTER
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0021 row: 0 column: 03
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

TITLE
JOURNAL
COMMENT
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location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5393 AAAAAATACAAAAAGAA 5411
1 AAAAAAAAAAAAAAAAAA 19
Db

RESULT 692 19 bp DNA linear GSS 16-FEB-2001
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LOCUS 2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0031H17 R, genomic survey sequence.
ACCESSION AZ786336
VERSION AZ786336.1 GI:12923992
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: H column: 17
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

TITLE
JOURNAL
COMMENT
FEATURES
SOURCE
location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD24nv; Purified genomic DNA from M.
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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5396 AAAAAATACAAAAAGAAAA 5414
Db 19 AAAAAAAAAAAGAAAAA 1

RESULT 693
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LOCUS 2M0034M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0034M12 F, genomic survey sequence.
ACCESSION AZ787634
VERSION AZ787634.1 GI:12926621
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: M column: 12
Seq primer: CATTCTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

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/organism="Mus musculus"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5393 AAAAAATACAAAAAGAAA 5411
Db 19 AAAAAAAAAAAGAAAAA 1

RESULT 694
AZ788058/c 19 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0034I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0034I24 R, genomic survey sequence.
ACCESSION AZ788058
VERSION AZ788058.1 GI:12927475
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: I column: 24
Seq primer: CACACAGGAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0034I24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 5393 AAAAAATACAAAAGAA 5411
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19 AAAAAAAAAAAAAAAAAA 1

RESULT 695
LOCUS AZ789590 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0037G06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0037G06 R, genomic survey sequence.
ACCESSION AZ789590
VERSION AZ789590.1 GI:12930573
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: G column: 06
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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/strain="C57BL/6J"
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/clone="UUGC2M0037G06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 5393 AAAAAATACAAAAGAA 5411
|||||
19 AAAAAAAAAAAAAAAAAA 1

RESULT 696
LOCUS AZ792713 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0045C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045C22 F, genomic survey sequence.
ACCESSION AZ792713
VERSION AZ792713.1 GI:12936930
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: C column: 22
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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/strain="C57BL/6J"
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/clone="UUGC2M0045C22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAGAA 5411
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 697
AZ795403 19 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0049C12R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0049C12 R, genomic survey sequence.

ACCESSION AZ795403
VERSION AZ795403.1 GI:12942392
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0049 row: C column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

Location/Qualifiers

1. 19
/organism="Mus musculus"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAGAA 5411
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 698
AZ801970 19 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0060112R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG2M0060112 R, genomic survey sequence.

ACCESSION AZ801970
VERSION AZ801970.1 GI:12954293
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0060 row: I column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

Location/Qualifiers

1. 19
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/clone="UGCG2M0060112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411
||||| | ||||| |
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 699
AZ822225 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0139G08R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCG2M0139G08 R, genomic survey sequence.
ACCESSION AZ822225
VERSION AZ822225.1 GI:12992133
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: E column: 17
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
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1..19
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/db_xref="taxon:10090"
/clone="UGCG2M0139G08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAAAAAAACAAAAAGAA 5411
||||| | ||||| |
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 700
AZ841581 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0139G08R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCG2M0139G08 R, genomic survey sequence.
ACCESSION AZ841581
VERSION AZ841581.1 GI:13011489
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: G column: 08
Seq primer: CACACAGAAACACATGAC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0139G08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
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adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|473214|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAAGAA 5411
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 701

AZ841622

LOCUS 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0139A16 R, genomic survey sequence.

AZ841622

Accession AZ841622.1 GI:13011530

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

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Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
Genome Center

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0139 row: A column: 16

Seq primer: CACACAGGAAACAGCTAGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

SOURCE

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0139A16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

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ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAAGAA 5411
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 702

AZ861896

LOCUS 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0168P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0168P10 R, genomic survey sequence.

AZ861896

Accession AZ861896.1 GI:13058674

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

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plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

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Genome Center

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0168 row: P column: 10

Seq primer: CACACAGGAAACAGCTAGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

SOURCE

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0168P10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

Query Match 0.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAAGAA 5411
 ||||| | ||||| |
 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 703
 AZ936798
 LOCUS 19 bp DNA linear GSS 26-APR-2001
 DEFINITION 2M0193L10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0193L10 R, genomic survey sequence.
 ACCESSION AZ936798
 VERSION AZ936798.1 GI:13795379
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0193 row: L column: 10
 Seq primer: CACACAGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
 source 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0193L10"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (g1[473214|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAAGAA 5411
 ||||| | ||||| |
 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 704
 AZ962226
 LOCUS 19 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0231A02 F, genomic survey sequence.
 ACCESSION AZ962226
 VERSION AZ962226.1 GI:13833453
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0231 row: A column: 02
 Seq primer: CGTTGTAAACGACGGCCAGCT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
 source 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0231A02"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (g1[473214|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 4e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5394 AAAAAAAAAAGAA 5412
 Db 1 AAAAAAAAAAAAAA 19

RESULT 705

A2985501

LOCUS 19 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0267E21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0267E21 F, genomic survey sequence.

ACCESSION A2985501

VERSION A2985501.1 GI:13856728

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0267 row: E column: 21

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0267E21"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g14732114[gbl|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAAAAAAGAA 5411
 Db 1 AAAAAAAAAAAAAA 19

RESULT 706

BH000498

LOCUS 19 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0288I21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0288I21 F, genomic survey sequence.

ACCESSION BH000498

VERSION BH000498.1 GI:13871724

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0288 row: I column: 21

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0288I21"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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polynucleotide kinase. Adaptor oligonucleotides were

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10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g14732114[gbl|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 4e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5393 AAAAATAACAAAAGAA 5411
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 707
AJ600883/c 19 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone
DEFINITION 515E07, genomic survey sequence.
ACCESSION AJ600883
VERSION AJ600883.1 GI:37950511
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
Brunaud,V., Balergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Dehose,R., Pelletier,G.,
Lepointec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL MEDLINE 22363535
PUBMED 12446535
REFERENCE 2 (bases 1 to 19)
AUTHORS Balergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
source
1. .19
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultiivar="Wassiljewskij'a"
/db_xref="taxon:3702"
/clone="515E07"
/clone_id="Arabidopsis thaliana T-DNA insertion lines"
1. .19
/note="T-DNA flanking sequence
right border"

misc_feature
Query Match 0.3%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5405 AAAAGAAAAATGAATA 5423
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Db 19 AAAACAAAGTTGAAATA 1

RESULT 708
CL680736 19 bp DNA linear GSS 09-JUL-2004
LOCUS PR1012a.H07_2 - PR1012a.BR (19) Note: Recurring String Mixed stage
DEFINITION foemid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL680736
VERSION CL680736.1 GI:50187696

KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE Appapd: an Acedb database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel.: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: foemid ends.
Location/Qualifiers
source
1. .19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_id="Mixed stage foemid library of P. pacificus
var. California"
/note="Vector: pDplfos-5 foemid vector"

Qy 5393 AAAAATAACAAAAGAA 5411
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Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 709
CL685439 19 bp DNA linear GSS 09-JUL-2004
LOCUS PR10141b.A04_2 - PR10141b.BR (19) Mixed stage foemid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL685439
VERSION CL685439.1 GI:50193696
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE Appapd: an Acedb database for the nematode satellite organism
JOURNAL Pristionchus pacificus
COMMENT Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel.: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: foemid ends.
Location/Qualifiers
source
1. .19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"

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/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage foemid library of P. pacificus
var. California"
/note="Vector: pepifos-5 foemid vector"

Query Match      0.3% Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 5393 AAAAAAATACAAAAAGAA 5411
||||| ||||| ||||| ||||| |||||
1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 710
LOCUS CL693186 19 bp DNA linear GSS 10-JUL-2004
DEFINITION PRI0160C.B05.2 - PRI0160C.BR (19) Note: Recurring String Mixed
stage foemid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL693186
VERSION CL693186
KEYWORDS GI:50215094
SOURCE GSS.
ORGANISM Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nemodiplogasteridae; Pristionchus.
1 (bases 1 to 19)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
Appadb: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: foemid ends.
Location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage foemid library of P. pacificus
var. California"
/note="Vector: pepifos-5 foemid vector"

FEATURES
source
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage foemid library of P. pacificus
var. California"
/note="Vector: pepifos-5 foemid vector"

Query Match      0.3% Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 711
LOCUS CL693191 19 bp DNA linear GSS 10-JUL-2004
DEFINITION PRI0160C.H08.2 - PRI0160C.BR (19) Note: Recurring String Mixed
stage foemid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL693191
VERSION CL693191
KEYWORDS GI:50215099
SOURCE GSS.
ORGANISM Pristionchus pacificus

```

```

ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nemodiplogasteridae; Pristionchus.
1 (bases 1 to 19)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
Appadb: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: foemid ends.
Location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage foemid library of P. pacificus
var. California"
/note="Vector: pepifos-5 foemid vector"

FEATURES
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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage foemid library of P. pacificus
var. California"
/note="Vector: pepifos-5 foemid vector"

Query Match      0.3% Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 5393 AAAAAAATACAAAAAGAA 5411
||||| ||||| ||||| ||||| |||||
1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 712
LOCUS AL038460 20 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZP5682246.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZP5682246, mRNA sequence.
AL038460
ACCESSION AL038460.1 GI:49682131
VERSION AL038460.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 20)
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gaassenhuber,U. and
Wiemann,S.
EST (Ottewaelder, et al.)
TITLE Unpublished (1999)
JOURNAL Contact: MIPS
AUTHORS MIPS
COMMENT MIPS
INGOLSTAEDTER Landstr.1, D-85764 Neuberg, Germany.
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP5682246"
/tissue_type="Kidney"
/dev_stage="fetal"
/clone_lib="X1-2blue"
/note="Vector: pMP1, Site.1: NotI, Site.2: SalI"

FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP5682246"
/tissue_type="Kidney"
/dev_stage="fetal"
/clone_lib="X1-2blue"
/note="Vector: pMP1, Site.1: NotI, Site.2: SalI"

Query Match      0.3% Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02; 3; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 5402 CAAAAAGAAAAATGAAA 5420
 Db 2 CAAAAAGAAAAATGAAA 20

RESULT 713
 AL587572/c
 LOCUS 20 bp mRNA linear EST 02-MAR-2001
 DEFINITION AL587572 BP Chicken Brain Library Gallus gallus cDNA clone
 ACCESSION AL587572
 VERSION AL587572.1 GI:13192606
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 20)
 REFERENCE
 AUTHORS Murray, F.
 TITLE BP Chicken Brain Library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Frazer Murray
 Dept. Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UK
 Tel: +44 (0)131 527 4200
 Fax: +44 (0)131 440 0434
 Email: frazer.murray@dbsrc.ac.uk
 GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
 (*6854-)

Seq primer: M13F.
 Location/Qualifiers
 1..20
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="ROS059B11"
 /tissue_type="Brain"
 /dev_stage="Unknown"
 /lab_host="DH10B"
 /clone_1lb="BP Chicken Brain Library"
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
 unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
 GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
 Clontech (*6854-1)"

Query Match 0.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5402 CAAAAAGAAAAATGAAA 5420
 Db 19 CAAAAAGAAAAATGAAA 1

RESULT 714
 AL587727/c
 LOCUS 20 bp mRNA linear EST 02-MAR-2001
 DEFINITION AL587727 BP Chicken Brain Library Gallus gallus cDNA clone
 ACCESSION AL587727
 VERSION AL587727.1 GI:13192761
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 20)
 REFERENCE
 AUTHORS Murray, F.

TITLE BP Chicken Brain Library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Frazer Murray
 Dept. Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UK
 Tel: +44 (0)131 527 4200
 Fax: +44 (0)131 440 0434
 Email: frazer.murray@dbsrc.ac.uk
 GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
 (*6854-)

Seq primer: M13F.
 Location/Qualifiers
 1..20
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="ROS061G06"
 /tissue_type="Brain"
 /dev_stage="Unknown"
 /lab_host="DH10B"

Query Match 0.3%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 4.2e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5398 AATACAAAAAGAAAAAT 5416
 Db 19 AAAAAAGAAAAAT 1

RESULT 715
 AL587759/c
 LOCUS 20 bp mRNA linear EST 02-MAR-2001
 DEFINITION AL587759 BP Chicken Brain Library Gallus gallus cDNA clone
 ACCESSION AL587759
 VERSION AL587759.1 GI:13192793
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 20)
 REFERENCE
 AUTHORS Murray, F.
 TITLE BP Chicken Brain Library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Frazer Murray
 Dept. Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UK
 Tel: +44 (0)131 527 4200
 Fax: +44 (0)131 440 0434
 Email: frazer.murray@dbsrc.ac.uk
 GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
 (*6854-)

Seq primer: M13F.
 Location/Qualifiers
 1..20
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="ROS061G06"
 /tissue_type="Brain"
 /dev_stage="Unknown"
 /lab_host="DH10B"

/clone.lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3', 3' adaptor sequence: 5'
GGGCCCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5398 AATACAAAGAAATGAAAT 5416

Db 19 AAAAAAAAAAAAAAAAAAT 1

RESULT 716
CF282002/c
LOCUS
DEFINITION
CF282002 20 bp mRNA linear EST 14-AUG-2003
14ETL--09-F01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F01,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
CF282002.1 GI:33659389

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 20)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..20
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-F01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone.lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5402 CAAAAAGAAATGAAA 5420

Db 20 CAAAAAAAAAAAAAAAAA 2

RESULT 717
CF299570/c
LOCUS
DEFINITION
CF299570 20 bp mRNA linear EST 15-AUG-2003
7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K09, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CF299570.1 GI:33671331
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 20)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..20
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-K09"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone.lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5390 ATTAAAAAATACAAAAA 5408

Db 19 AGTAAAAAAAAAAAAAAAAA 1

RESULT 718
CF316662/c
LOCUS
DEFINITION
CF316662 20 bp mRNA linear EST 15-AUG-2003
HD--06-A20.g1 OshDACL-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-A20, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CF316662.1 GI:33688423
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
1 (bases 1 to 20)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..20
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"

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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-A20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="vector: PCR4-TOP0, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5402 CAAAAGAAAATGAAA 5420
Db      ||||| ||||| |||
        19 CAAAAAATAAAAAA 1

RESULT 719
CF318278/c 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-08-F13.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD-08-F13, mRNA sequence.
ACCESSION  CF318278
VERSION     CF318278.1 GI:33690039
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr.
            location/Qualifiers
FEATURES
SOURCE
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-F13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="vector: PCR4-TOP0, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5393 AAAAAATACAAAAAGA 5411
Db      ||||| ||||| |||
        19 CAAAAAATAAAAAA 1
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Db      20 AAAAAAATAAAAAA 2
        ||||| ||||| |||

RESULT 720
CF319428/c 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-09-O20.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD-09-O20, mRNA sequence.
ACCESSION  CF319428
VERSION     CF319428.1 GI:33691189
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr.
            location/Qualifiers
FEATURES
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1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-O20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="vector: PCR4-TOP0, Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5391 TTAATAAATACAAAAAG 5409
Db      ||||| ||||| |||
        19 TCAAAAAAATAAAAAAG 1

RESULT 721
CF320843/c 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-11-001.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD-11-001, mRNA sequence.
ACCESSION  CF320843
VERSION     CF320843.1 GI:33692604
KEYWORDS   EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS
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TITLE Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

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1. .20
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/mol_type="mRNA"
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/clone="HD-11-001"
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/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5402 CAAAGAAAGAAAATGAAA 5420
|||||
20 CAAAAAAAAAAAAAAAAAAAA 2

RESULT 722

AZ68518

LOCUS 20 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0118G09R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0118G09 R, genomic survey sequence.

ACCESSION AZ68518

VERSION A268518.1 GI:10482218

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiser
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0118 row: G column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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1. .20
/organism="Mus musculus"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0118G09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

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/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5389 AATTAAAAAATACAAAA 5407
|||||
2 ATTAAAAAAAAACAAAA 20

RESULT 723

AZ626475

LOCUS 20 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0466E16R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0466E16 R, genomic survey sequence.

ACCESSION AZ626475

VERSION A2626475.1 GI:11748665

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiser
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0466 row: E column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UGC1M0466E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4606 CAGTGTGAGCCGAGAGC 4624
DB 19 CCGCGCTGAGCCGAGAGC 1

RESULT 724
LOCUS AZ638704 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0498E13R Mouse 10kb plasmid UGC1M library Mus musculus genomic
ACCESSION AZ638704
VERSION AZ638704.1 GI:11760894
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: B column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

/db_xref="taxon:10090"
/clone="UGC1M0498E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAGAA 5411
DB 2 AAAAAAAAAAAAAAAAAA 20

RESULT 725
LOCUS AZ821905 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0094D20R Mouse 10kb plasmid UGC1M library Mus musculus genomic
ACCESSION AZ821905
VERSION AZ821905.1 GI:12991813
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

/clone="UUGC2M0094D20"
/sex="Male"
/lab host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3% Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2% Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5402 CAAAAAGCAAAATGAAA 5420

Db 2 CAAAAAGCAAAATGAAA 20

RESULT 726
AM248574/c 17 bp mRNA linear EST 07-JAN-2000
LOCUS 2821096.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821096 3',
DEFINITION mRNA sequence.

ACCESSION AM248574
VERSION AM248574.1 GI:6591567
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS 1 (bases 1 to 17)
TITLE NIH-MGC http://mgs.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Other_ESTRs: 2821096.5prime
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing

Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

www-bio.lnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu/Low Quality Sequence: 8 contiguous

PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks

following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L10M5 row: 0 column: 17
High quality sequence stop: 8.
Location/Qualifiers
1..17
Location="Homo sapiens"

Query Match 0.3% Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2% Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5396 AAAATACAAAAAGAAA 5412

Db 17 AAAATACAAAAAGAAA 1

RESULT 727
BQ590128/c 17 bp mRNA linear EST 06-DEC-2002
LOCUS E012843-024-019-E19-T7 MP12-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-019-E19-3-PRIME, mRNA sequence.

ACCESSION BQ590128
VERSION BQ590128.1 GI:26119711
KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 17)
Hertwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)
22362189
12472698

COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weisshaar@mplz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00

Plate: 19 row: B column: 19
Seq primer: T7; GTATACGATCACTATAGGCG.

Location/Qualifiers
1..17
Location="Beta vulgaris"

/mol type="mRNA"
/culivar="KWS2320 (double haploid, monogerm breeding

line)"
/db_xref="GABI:189986"

/db_xref="taxon:161934"
/clone="024-019-E19"

/issue type="storage root"
/lab host="EMDH10B"

/clone_lib="MP12-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Eibbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5392 TAAATACCAAAAGAAAA 5408
17 TAAAAAAAAAAAAAAAAA 1

RESULT 728
B0591181/c
LOCUS
DEFINITION B0591181 17 bp mRNA linear EST 06-DEC-2002
E012715-024-017-H16-T7 MP12-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-H16 3-PRIME, mRNA sequence.

ACCESSION B0591181
VERSION B0591181
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 17 Std Error: 0.00
Plate: 17 Row: H Column: 16
Seq primer: T7; GATATACGACTCACTATAGGCGC.
Location/Qualifiers

FEATURES
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1. .17
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/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188932"
/db_xref="taxon:161934"
/clone="024-017-H16"
/issue_type="storage root"
/lab_host="BMDH10B"
/note="Vector: PCMVSPOR6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzehnleberer Saatnucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5399 ATACAAAAAGAAAA 5415
17 AAAAAAAAAAAAAAAAAA 1

RESULT 729
CF276637
LOCUS
DEFINITION CF276637 17 bp mRNA linear EST 14-AUG-2003
14ETL--01-N18.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) CDNA clone 14ETL--01-N18,
mRNA sequence.

ACCESSION CF276637
VERSION CF276637
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretaceae; Oryzae; Oryza.
1 (bases 1 to 17)
Kim,Y.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--01-N18"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5397 AATACAAAAAGAAAA 5413
1 AAAAAAAAAAAAAAAAAA 17

RESULT 730
CF294668/c
LOCUS
DEFINITION CF294668 17 bp mRNA linear EST 14-AUG-2003
30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) CDNA clone 30DGS--04-E17, mRNA
sequence.

ACCESSION CF294668
VERSION CF294668
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretaceae; Oryzae; Oryza.
1 (bases 1 to 17)
Kim,Y.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--04-E17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5392 TAAATAATACAAAAA 5408
Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 731
CF295988 17 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
ACCESSION CF295988
VERSION CF295988.1 GI:33665021
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--06-C17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

RESULT 733
CF336950 17 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--07-D04.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-D04, mRNA sequence.
ACCESSION CF336950
VERSION CF336950.1 GI:33822280
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5392 TAAATAATACAAAAA 5408
Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 732
CF319075 17 bp mRNA linear EST 15-AUG-2003
LOCUS HD--09-H06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H06, mRNA sequence.
ACCESSION CF319075
VERSION CF319075.1 GI:33690836
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice histone Deacetylase overexpression
line."

Query Match 0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5399 ATACAAAAAGAAAAA 5415
Db 17 ATAAAAAAAAAAAAAAAAA 1

RESULT 733
CF336950 17 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--07-D04.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-D04, mRNA sequence.
ACCESSION CF336950
VERSION CF336950.1 GI:33822280
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

```

ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE      Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Euhartoideae; Oryzaceae; Oryza.
TITLE          1 (bases 1 to 17)
JOURNAL        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
                Location/Qualifiers
                1..17
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="JMT--07-D04"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="ACUMT-overexpressing transgenic rice plasmid
                cDNA library (JMT)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
                was reverse transcribed and then used for PCR. mRNA was
                prepared from Arabidopsis Jasmonate Carboxyl
                methyltransferase overexpression line."

Query Match      0.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5392 TAAAAAATTCAAAAA 5408
Db      17 TAAAAAATTCAAAAA 1

RESULT 734
CF302409/c      18 bp      mRNA      linear      EST 15-AUG-2003
LOCUS          7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA
                sequence.
ACCESSION      CF298591
VERSION        CF298591
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
                Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Euhartoideae; Oryzaceae; Oryza.
                1 (bases 1 to 18)
                Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
                Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
                Location/Qualifiers
                1..18
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                /mol_type="mRNA"
                /cultivar="Nackdong"
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                /clone="7LEAF--05-005"
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                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                with oligoribonucleotides and then used as templates for
                RT-PCR."

FEATURES
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FEATURES
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Query Match      0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5391 TTTAAAAAATTCAAAAA 5407
Db      17 TTTAAAAAATTCAAAAA 1

RESULT 735
CF301151/c      18 bp      mRNA      linear      EST 15-AUG-2003
LOCUS          7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone 7LEAF--05-005, mRNA
                sequence.
ACCESSION      CF301151
VERSION        CF301151.1 GI:33672912
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
                Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                1 (bases 1 to 18)
                Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
                Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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                /lab_host="E.coli DH10B"
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                with oligoribonucleotides and then used as templates for
                RT-PCR."

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FEATURES
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1..18
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Accession      CF302409     GI:33674170
Version        CF302409.1
Keywords       EST.
Source         Oryza sativa (japonica cultivar-group)
Organism       Oryza sativa (japonica cultivar-group)
Reference      Oryza sativa (japonica cultivar-group)
Authors        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoidae; Oryzaceae; Oryza.
Title          1 (bases 1 to 18)
Journal        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Comment        Large-scale Sequencing Analysis of Rice ESTs
               Unpublished (2003)
               Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of BioScience and Bioinformatics, Myoungji University
               Yongin, Kyeonggi, Korea
               Tel.: 82 31 321 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
               Location/Qualifiers
                 location="Oryza sativa (japonica cultivar-group)"
                 mol_type="mRNA"
                 /cultiyar="Nackdong"
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                 /issue_type="leaf"
                 /dev_stage="7 days after germination"
                 /lab_host="E.coli DH10B"
                 /clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"
                 /note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
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               RT-PCR."

Query Match    0.3%; Score 13.8; DB 1; Length 18;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db            17 TAAAAAAAAAAAAAAAAA 1
||||| | |||||
||||| | |||||

RESULT 737
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DEFINITION    HD-10-M11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
               library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
               HD-10-M11, mRNA sequence.
ACCESSION     CF320046
VERSION       CF320046.1 GI:33691807
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoidae; Oryzaceae; Oryza.
TITLE         1 (bases 1 to 18)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
COMMENT       Large-scale Sequencing Analysis of Rice ESTs
               Unpublished (2003)
               Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of BioScience and Bioinformatics, Myoungji University
               Yongin, Kyeonggi, Korea
               Tel.: 82 31 321 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
               Location/Qualifiers

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source
1. 18
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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cdna library (HD)"
/name="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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cdna library (HD)"
|/name="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
|treated with ABA(20um) for 1hr. Oligo-capped mRNA was
|reverse transcribed and then used for PCR. mRNA was
|derived from rice Histone Deacetylase overexpression
|line."

Db 18 ATAAAAAAGAAAAA 2

RESULT 738
LOCUS CF320418/C
DEFINITION HD-11-E22_g1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cdna clone
HD-11-E22, mRNA sequence.
CF320418
CF320418 GI:33692179
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 18
/organism="Oryza sativa (japonica cultivar-group)"
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
Source
Query Match 0.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 5393 AAAAAAAAAACAAAAG 5409
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 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 739
 CF278272/c
 LOCUS 19 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 ORYZA SATIVA (japonica cultivar-group) cDNA clone 14ETL--04-C01,
 mRNA sequence.
 CF278272
 ACCESSION CF278272.1 GI:33655658
 VERSION EST.
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
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 RT-PCR."

Query Match 0.3%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5391 TTAATAAATGACAAA 5407
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 Db 17 TTAATAAATGACAAA 1

RESULT 740
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 LOCUS 19 bp DNA linear GSS 02-OCT-2000
 DEFINITION IM0103G03R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0103G03 R, genomic survey sequence.
 AZ360314
 ACCESSION AZ360314.1 GI:10474014
 VERSION GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE Niederhausern,A. and Wright D.,Weiss,R.
 JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0103 row: G column: 03
 Seq primer: CACACAGAAACACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1fb="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (g14732114[gblAF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E.coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5409 GAAAAAATGAAATTA 5425
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 Db 1 GAAAAAATGAAATTA 17

RESULT 741
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 LOCUS 19 bp DNA linear GSS 03-OCT-2000
 DEFINITION IM0218L14F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0218L14 F, genomic survey sequence.
 AZ432757
 ACCESSION AZ432757.1 GI:10556770
 VERSION GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0218 row: L column: 14
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUC1M0218L14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gil4732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
source

Query Match 0.3%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2568 GGAGAGAGAGATCGAGA 2584
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1 GGAGAGCGAGAGCGAGA 17

Db 1

RESULT 742
LOCUS AZ447251 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0244J19F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0244J19 F, genomic survey sequence.
ACCESSION AZ447251
VERSION AZ447251.1 GI:10599050
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: J column: 19
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gil4732114[gb]|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
source

Query Match 0.3%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5399 ATACAAAAGAGAAAAA 5415
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17 ATAAAAAAGAGAAAAA 1

Db 17

RESULT 743
LOCUS AZ450180 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0248K13R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0248K13 R, genomic survey sequence.
ACCESSION AZ450180
VERSION AZ450180.1 GI:10604710
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gdbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES

source

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1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14R07-01-E19"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14R07)"
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RT-PCR."
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Qy 5393 AAAAAAAAAACAAAA 5407
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 Db 1 AAAAAAAAAAAAAA 15

RESULT 748
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 DEFINITION cDNA clone 024-026-123 5-PRIME, mRNA sequence.
 ACCESSION BQ593528
 VERSION BQ593528.1 GI:26123111
 KEYWORDS EST.

SOURCE

ORGANISM

Beta vulgaris
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 17)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Dzungowski,M., Stahl,D., Wruck,W., Mene,A., O'Brien,J., Lebrach,H.
 and Kadelof,U.

REFERENCE

AUTHORS

Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

JOURNAL

22362189

PUBMED

12472698

COMMENT

Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 26 Row: 1 Column: 23
 Seq primer: SP6; CATACGATTAGCTGACACTATAG.
 Location/Qualifiers

FEATURES

source

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1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:193326"
/db_xref="taxon:161934"
/clone="024-026-123"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/notes="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinanzelebener Saatzzucht AG Einbeck, Germany, contact:
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b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-beet
 project, local PI: Dr. Katharina Schneider, coordinator;
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 4.5e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1181 GAGAAAGAGAGAG 1195
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 Db 15 GAGAGAGAGAGAG 1

RESULT 749
 BM658677/c 18 bp mRNA linear EST 27-FEB-2002
 LOCUS LVV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
 DEFINITION sequence.
 ACCESSION BM658677
 VERSION BM658677.1 GI:18958948
 KEYWORDS EST.

SOURCE

Sus scrofa (pig)
 Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

AUTHORS

Unpublished (2002)
 Porcine EST
 Contact: David L. Adelson
 Animal Breeding and Genetics
 Texas A&M University
 Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
 USA
 Tel: 9798452616
 Fax: 9798456970
 Email: david.adelson@amu.edu.

FEATURES

source

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1. .18
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone_lib="CSEQFXL37 pig adrenal"
/notes="Organ: adrenal gland; Vector: pBluescript SK+;
Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GCCAATTGAGCTCACCGGCGGCGCGCGCGCTCGAG. Sequence 3' of
the inserts (AAGAATTCGATATCACTTATCGATACCGTCGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."
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Query Match 0.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 4.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5401 ACAGAGAGAGAG 5415
 |||||
 Db 17 AAGAGAGAGAGAG 3

RESULT 750
 AZ447864/c 19 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0245A14F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 DEFINITION clone UUC1M0245A14 F, genomic survey sequence.
 ACCESSION AZ447864
 VERSION AZ447864.1 GI:10600087
 KEYWORDS GSS.

SOURCE

Mus musculus (house mouse)
 Mus musculus

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0245 row: A column: 14
Seq primer: CGTGTAAACACACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0245A14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114[gblAf129072.1]), a copy-number inducible derivative of Plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5411 AAAAATGAATAATAA 5425
17 AAAAATGAATAATAA 3

RESULT 751
LOCUS

AL038692 18 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZ566J0846_r1.566 (synonym: hfk42) Homo sapiens cDNA clone
DKFZ566J0846_mRNA sequence.

ACCESSION AL038692.1 GI:49682190

VERSION AL038692.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 18)
Ostenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Ostenwaelder, et al.)
Unpublished (1999)
Contact: MIPS

TITLE

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

JOURNAL
COMMENT

Unpublished (1999)
Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ566J0846"
/cissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfk42)"
/note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

QY 5398 AATCAAAAAGAAAAA 5415
17 AAAAAAAAAAAAAAAAAA 18

RESULT 752
LOCUS

AL048754 18 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZ566L173_r1.566 (synonym: hfk42) Homo sapiens cDNA clone
DKFZ566L173_mRNA sequence.

ACCESSION AL048754
VERSION AL048754.1 GI:4727825

KEYWORDS

EST.
Homo sapiens (human)

SOURCE

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 18)
Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehler, et al.)
Unpublished (1999)
Contact: MIPS

TITLE

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

JOURNAL
COMMENT

Unpublished (1999)
Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ566L173"
/cissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfk42)"
/note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

QY 5391 TTAATAAATACAAAAA 5408
1 TCAAAAAAAAAAAAAAAAAA 18

RESULT 753
LOCUS AM246505/C 18 bp mRNA linear EST 07-JAN-2000

DEFINITION 2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3', mRNA sequence.

ACCESSION AM246505

VERSION AM246505.1 GI:6589498

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE NIH-MGC

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Other ESTs: 2821585.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing project

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://www.genome.washington.edu/LowQualitySequence>

contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LHCW7 row: D column: 2

High quality sequence stop: 18.

Location/Qualifiers

1. 18

/organism="Homo sapiens"

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/clone="IMAGE:2821585"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_7"

/note="Organ: Lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5397 AATACCAAAAGAAAAA 5414

Db 18 AATTAAGAAAAA 1

RESULT 754

BO582676 18 bp mRNA linear EST 06-DEC-2002

LOCUS BO582676/c

DEFINITION cDNA clone 024-007-P18-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris

ACCESSION BO582676

VERSION BO582676.1 GI:26112253

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE Herwig,R., Schultz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE

PUBMED 22362189

12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 18 Std Error: 0.00

Plate: 7 row: P column: 18

Seq primer: SP6; CATACGATTAGCTGACACTATAG.

Location/Qualifiers

1. 18

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KMS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:184018"

/db_xref="taxon:161934"

/clone="024-007-P18"

/tissue_type="inflorescence"

/lab_host="EMDH10B"

/clone_id="MP1Z-ADIS-024-inflorescence"

/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzehnlebeher Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCAGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5398 AATCAAAAGAAAAA 5415

Db 18 AAAAAA 1

RESULT 755

BO590027 18 bp mRNA linear EST 06-DEC-2002

LOCUS BO590027/c

DEFINITION E012844-024-019-E24-T7 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION BO590027

VERSION BO590027.1 GI:26119610

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE Herwig,R., Schultz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE

PUBMED 22362189

12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 18 Std Error: 0.00

Plate: 7 row: P column: 18

Seq primer: SP6; CATACGATTAGCTGACACTATAG.

Location/Qualifiers

1. 18

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KMS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:184018"

/db_xref="taxon:161934"

/clone="024-007-P18"

/tissue_type="inflorescence"

/lab_host="EMDH10B"

/clone_id="MP1Z-ADIS-024-inflorescence"

/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzehnlebeher Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCAGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

LOCUS CF299027 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-N14, mRNA sequence.
 ACCESSION CF299027
 VERSION CF299027.1 GI:33670788
 KEYWORDS EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriarthroideae; Oryzaceae; Oryza.
 1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. 18
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--02-N14"
 /issue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5398 AATCAAAAAAGAAAAA 5415
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 759
 CF299674/c 18 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-M14, mRNA sequence.
 ACCESSION CF299674
 VERSION CF299674.1 GI:33671435
 KEYWORDS EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriarthroideae; Oryzaceae; Oryza.
 1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355

FEATURES
 source Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. 18
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--03-M14"
 /issue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5398 AATCAAAAAAGAAAAA 5415
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 760
 CF300456/c 18 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N23, mRNA sequence.
 ACCESSION CF300456
 VERSION CF300456.1 GI:33672217
 KEYWORDS EST.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriarthroideae; Oryzaceae; Oryza.
 1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. 18
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--04-N23"
 /issue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5408 AGAAAAATGAAATATA 5425
 Db 18 AGAAAAAAAAAAAAAAAA 1

RESULT 761
CF301325/c
LOCUS
DEFINITION

CF301325 18 bp mRNA linear EST 15-AUG-2003
7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-C12, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF301325
CF301325.1 GI:33673086
EST.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-C12"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3;

Oy 5398 AATCAAAAAGAAAAA 5415
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 762
CF301760/c
LOCUS
DEFINITION

CF301760 18 bp mRNA linear EST 15-AUG-2003
7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L22, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF301760
CF301760.1 GI:33673521
EST.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-L22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3;

Oy 5398 AATCAAAAAGAAAAA 5415
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 763
CF309376/c
LOCUS
DEFINITION

CF309376 18 bp mRNA linear EST 15-AUG-2003
ABF--03-119.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--03-119, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF309376
CF309376.1 GI:33681137
EST.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--03-119"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried
for 2hrs. Oligo capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5398 AATACAAAAAGAAAAA 5415
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 18 AGTAAAAA 1

Db 18 AGTAAAAA 1

RESULT 764
 CF329484/c 18 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA
 sequence.
 ACCESSION CF329484 GI:33807207
 VERSION CF329484
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Bkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Oryza sativa (japonica cultivar-group)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..18
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--04-N06"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5398 AATACAAAAAGAAAAA 5415
 |||||
 18 AGTAAAAA 1

Db 18 AGTAAAAA 1

RESULT 765
 CF329485 18 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA
 sequence.
 ACCESSION CF329485 GI:33807209
 VERSION CF329485
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Bkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..18
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--04-N06"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5398 AATACAAAAAGAAAAA 5415
 |||||
 1 AGTAAAAA 18

Db 1 AGTAAAAA 18

RESULT 766
 AZ432757/c 19 bp DNA linear GSS 03-OCT-2000
 LOCUS IM0218L14F Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCGM0218L14 F, genomic survey sequence.
 ACCESSION AZ432757
 VERSION AZ432757.1 GI:10556770
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0218 row: L column: 14
 Seg primer: CGTTGTAAACGACGCGCAGCT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"

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/db_xref="taxon:10090"
/clone="U0GCM0218L14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U0GCM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.2%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      229  CCTCACCTCACCCTCC 246
Db      19  CCTCTCCTCTCCTCTC 2

RESULT 767
A1590540      16 bp  mRNA  linear  EST 14-MAY-1999
LOCUS      tw11c02.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:225362 3'
DEFINITION      similar to TR:000599 000599 CON1.; mRNA sequence.
ACCESSION      A1590540
VERSION      A1590540.1 GI:4599588
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 16)
NCI/NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGA), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/MLML at:
www-bio.1nl.gov/bbrp/image/image.html

FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="mRNA"

```

```

/db_xref="taxon:9606"
/clone="IMAGE:2259362"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn52"
/notes="Organ: brain; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; This library represents the normalized
version of NCI CGAP Brn5. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.19 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, astrocytoma (grade IV).
Constructed by Life Technologies."

Query Match      0.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1270  CCCGACCCACCCACC 1282
Db      3  CCCGACCCACCCACC 15

RESULT 768
A1569544      16 bp  mRNA  linear  EST 12-MAY-1999
LOCUS      to28d10.x1 NCI CGAP ut4 Homo sapiens cDNA clone IMAGE:2180371 3'
DEFINITION      similar to TR:Q18444 Q18444 COSMID C34D4.; contains MSRI.b2 MSRI
repetitive element.; mRNA sequence.
ACCESSION      A1569544
VERSION      A1569544.1 GI:4532918
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 16)
NCI/NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/MLML at:
www-bio.1nl.gov/bbrp/image/image.html

FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2180371"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP ut4"
/notes="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

Query Match      0.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5e+02;

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 227 CCCCTCACTCACC 242
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 Db 1 CCCCTCCCCCACC 16

RESULT 769
 B0590166/c 16 bp mRNA linear EST 06-DEC-2002
 LOCUS DEFINITION B012844-024-019-K18-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 B0590166 CNA clone 024-019-K18 3-PRIME, mRNA sequence.
 ACCESSION B0590166
 VERSION B0590166.1 GI:26119749
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 16)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lebrach,H.
 and Radehof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 MEDLINE
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 16 Std Error: 0.00
 Plate: 19 row: K column: 18
 Seq primer: T7; GTAATGACTCACTATGAGGC.
 Location/Qualifiers
 1..16
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiVar="KMS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:189955"
 /db_xref="taxon:161934"
 /clone="024-019-K18"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: PCMVSPORT6; Site 1: SalI, Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebeener Saat-zucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7. Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAA 5408
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 Db 16 AAAAAAAAAAAAAA 1

RESULT 770
 B0590507/c 16 bp mRNA linear EST 06-DEC-2002
 LOCUS DEFINITION B0590507

DEFINITION E012844-024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 CNA clone 024-019-M04 3-PRIME, mRNA sequence.
 B0590507
 B0590507.1 GI:26120090
 EST.
 Beta vulgaris
 Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 16)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lebrach,H.
 and Radehof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 MEDLINE
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 16 Std Error: 0.00
 Plate: 19 row: M column: 04
 Seq primer: T7; GTAATGACTCACTATGAGGC.
 Location/Qualifiers
 1..16
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 /mol_type="mRNA"
 /cultiVar="KMS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:189608"
 /db_xref="taxon:161934"
 /clone="024-019-M04"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: PCMVSPORT6; Site 1: SalI, Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebeener Saat-zucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7. Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5400 TACAAAAGAAAAA 5415
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 Db 16 TAAAAAAAAAAAAA 1

RESULT 771
 B0592600 16 bp mRNA linear EST 06-DEC-2002
 LOCUS DEFINITION B013686-024-028-F08-SP6R MP1Z-ADIS-024-developing root Beta
 vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
 B0592600
 B0592600.1 GI:26122183
 EST.
 Beta vulgaris
 Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT
 Contact: Weisshaar B
 ADIS DNA core facility at MPiZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 16 Std Error: 0.00
 Plate: 28 row: F column: 08
 Seq primer: SP6r: ATTAGTGCACCTATAGAGC.
 Location/Qualifiers
 1..16
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:194262"
 /db_xref="taxon:161934"
 /clone="024-028-F08"
 /tissue_type="developing root"
 /lab_host="EMDH108"
 /clone_lib="MPiZ-ADIS-024-developing root"
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebener Saat-zucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 5e+02; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5393 AAAAAAAAAACAAAAA 5408
 ||||| | |||||
 Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 772
 B0592965/c 16 bp mRNA linear EST 06-DEC-2002
 LOCUS S013317-024-028-A01-T7 MPiZ-ADIS-024-developing root Beta vulgaris
 DEFINITION cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
 ACCESSION B0592965.1
 VERSION B0592965.1 GI:26122548
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 16)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT
 Contact: Weisshaar B

ADIS DNA core facility at MPiZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
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 Seq primer: T7: GTAATAGCACTACTATAGGCG.
 Location/Qualifiers
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 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebener Saat-zucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 5e+02; Indels 0; Gaps 0;
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OY 5393 AAAAAAAAAACAAAAA 5408
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 Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 773
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 DEFINITION cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
 ACCESSION B0595369.1
 VERSION B0595369.1 GI:26124952
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 16)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT
 Contact: Weisshaar B
 ADIS DNA core facility at MPiZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
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/notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzzucht AG Eibbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Query Match 0.2%; Score 12.8; DB 1; Length 16;
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 DB 16 TAAAAAAGAAAAA 1

RESULT 774

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 ACCESSION B0595717
 VERSION B0595717
 KEYWORDS B0595717.1 GI:26125300
 SOURCE EST.
 ORGANISM Beta vulgaris

Beta vulgaris
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drunowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 JOURNAL plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698

COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp12-koeln.mpg.de
 Insert Length: 16 Std Error: 0.00
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/notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzzucht AG Eibbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Query Match 0.2%; Score 12.8; DB 1; Length 16;
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 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAAATACAAAAA 5408
 DB 1 AAAAAAAGAAAAA 16

RESULT 775
 LOCUS CF279325/C 16 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
 mRNA sequence.

ACCESSION CF279325
 VERSION CF279325.1 GI:33656711
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriarthroideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

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 DB 16 AAAAAAAGAAAAA 1

RESULT 776
 CF296130/C

LOCUS CF296130 16 bp mRNA linear EST 14-AUG-2003
 DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA sequence.
 ACCESSION CF296130
 VERSION CF296130.1 GI:33665163
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 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiaceae; Oryzae; Oryza.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
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 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5400 TACCAAAAGCAAAA 5415
 Db 16 TAAAAAAAAAAAAA 1

RESULT 777
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 DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--06-C03, mRNA sequence.
 ACCESSION CF311057
 VERSION CF311057.1 GI:33682818
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiaceae; Oryzae; Oryza.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

FEATURES
 source Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
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Query Match 0.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 5e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5393 AAAAAATACAAAAA 5408
 Db 16 AAAAAAAAAAAAAA 1

RESULT 778
 LOCUS CF314013 16 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--02-G01.g1 OsHDA1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--02-G01, mRNA sequence.
 ACCESSION CF314013
 VERSION CF314013.1 GI:33685774
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiaceae; Oryzae; Oryza.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
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 /lab_host="E.coli DH10B"
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Best Local Similarity 87.5%; Pred. No. 5e+02; DB 1; length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5400 TACAAAAAGAAAAA 5415

Db 16 TAAAAAAGAAAAA 1

RESULT 779

CF314377/c

LOCUS HD-02-001.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD-02-001, mRNA sequence.

ACCESSION CF314377

VERSION CF314377.1 GI:33686138

KEYWORDS EST.

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 12.8; DB 1; length 16;

Best Local Similarity 87.5%; Pred. No. 5e+02; DB 1; length 16;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAATACAAAAA 5408

Db 16 AAAAAAAGAAAAA 1

RESULT 780

CF315789/c

LOCUS HD-04-N10.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD-04-N10, mRNA sequence.

ACCESSION CF315789

VERSION CF315789.1 GI:33687550

KEYWORDS EST.

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 12.8; DB 1; length 16;

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 781

CF316056/c

LOCUS HD-05-D07.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD-05-D07, mRNA sequence.

ACCESSION CF316056

VERSION CF316056.1 GI:33687817

KEYWORDS EST.

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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/cultiyar="Nackdong"
/db_xref="taxon:39947"

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cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match	0.2%;	Score 12.8;	DB 1;	Length 16;
Best Local Similarity	87.5%;	Pred. No. 5e+02;	2;	Indels 0;
Matches	14;	Conservative	0;	Mismatches

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 16 AAAAAAAAAAAAAAAAAA 1

RESULT 782
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 HD--07-I05.g1 OSHDACT1-overexpressing transgenic rice plasmid cDNA
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 HD--07-I05, mRNA sequence.
 CF317718
 EST.
 CF317718.1 GI:33689479
 ORIGIN
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 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Erihartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
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 /cultivar="Nackdong"
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 cDNA library (HD)"
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 derived from rice Histone Deacetylase overexpression
 line."

Query Match	0.2%;	Score 12.8;	DB 1;	Length 16;
Best Local Similarity	87.5%;	Pred. No. 5e+02;	2;	Indels 0;
Matches	14;	Conservative	0;	Mismatches

OY 5393 AAAAAAAAAATCAAAAAA 5408
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 16 AAAAAAAAAAAAAAAAAA 1

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	Source
CF320356/c	HD--11-D14.b1 Oryza sativa (japonica cultivar-group) cDNA clone	CF320356											
LOCUS	16 bp mRNA linear EST 15-AUG-2003												
DEFINITION	HD--11-D14.b1 Oryza sativa (japonica cultivar-group) cDNA clone												
ACCESSION	HD--11-D14, mRNA sequence.												
VERSION													
KEYWORDS													
SOURCE													
ORGANISM													
REFERENCE													
AUTHORS													
TITLE													
JOURNAL													
COMMENT													
FEATURES													
Source													
Query Match	0.2%; Score 12.8; DB 1; Length 16;												
Best Local Similarity	87.5%; Pred. No. 5e+02;												
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;												
Oy	5393 AAAAAAAAAACAAAAA 5408												
Db	16 AAAAAAAAAAAAAAAAAA 1												
RESULT 784													
LOCUS	CF327722/c												
DEFINITION	NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA sequence.												
ACCESSION	CF327722												
VERSION	CF327722												
KEYWORDS													
SOURCE													
ORGANISM													
REFERENCE													
AUTHORS													
TITLE													
JOURNAL													
COMMENT													
FEATURES													
Source													
Query Match	0.2%; Score 12.8; DB 1; Length 16;												
Best Local Similarity	87.5%; Pred. No. 5e+02;												
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;												
Oy	5393 AAAAAAAAAACAAAAA 5408												
Db	16 AAAAAAAAAAAAAAAAAA 1												
RESULT 784													
LOCUS	CF327722												
DEFINITION	NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA sequence.												
ACCESSION	CF327722												
VERSION	CF327722												

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

SOURCE

Location/Qualifiers

1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-F06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;

OY 5393 AAAAAAATACAAAAA 5408

Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 785

CF329320/c 16 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
sequence.

ACCESSION CF329320.1 GI:33806877
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

SOURCE

Location/Qualifiers

1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="NACL--04-J17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 12.8; DB 1; Length 16;

Best Local Similarity 87.5%; Pred. No. 5e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;

OY 5400 TACAAAAAGAAAAA 5415

Db 16 TAAAAAAAAAAAAAAAAA 1

RESULT 786

CF333386 16 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-E05, mRNA sequence.

ACCESSION CF333386.1 GI:33815044
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

SOURCE

Location/Qualifiers

1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-E05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;

OY 5393 AAAAAAATACAAAAA 5408

Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 787

AW247165/c 17 bp mRNA linear EST 07-JAN-2000
LOCUS 2819675.jprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819675 3',
DEFINITION mRNA sequence.

ACCESSION AW247165.1 GI:6590158
VERSION
KEYWORDS
SOURCE
ORGANISM

EST. Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 17)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTRs: 2819675, 5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgsabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DIR CDNA Library Preparation: Ling
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LBNL) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LBNL at:
www.bic.lnlnl.gov/bbrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-T identification: patch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu> Low Quality Sequence: 17
 contiguous PHRED high quality bases following vector sequence. Very
 low Quality Sequence: Trace file contained 17 contiguous distinct
 peaks following vector sequence.
 Plate: LHCN2 row: D column: 12
 High quality sequence scop: 17.
 Location/Qualifiers

FEATURES

source

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/clone="IMAGE:2819675"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH-MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 0.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.2e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5397 AAATACAAAAGAAA 5412

DB 17 AAAAACAAAAGAAA 2

RESULT 788
BO590687 17 bp mRNA linear EST 06-DEC-2002
LOCUS SO13717-024-018-B24-T7 MP12-ADIS-024-storage root Beta vulgaris
DEFINITION CDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION BO590687
VERSION BO590687.1 GI:26120270
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
 Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mp12-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 18 row: B column: 24
 Seq primer: T7; GTAATACGACTCACTATAGGCG.
 Location/Qualifiers

FEATURES

source

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1..17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189432"
/db_xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Bindeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Query Match 0.2%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.2e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5393 AAAAATACAAAAGAAA 5408

DB 1 AAAAATACAAAAGAAA 16

RESULT 789
BO591177 17 bp mRNA linear EST 06-DEC-2002
LOCUS BO591177/c
DEFINITION E013715-024-017-B22-T7 MP12-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-B22 3-PRIME, mRNA sequence.
ACCESSION BO591177
VERSION BO591177.1 GI:26120760
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
 Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mp12-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 17 row: B column: 22
 Seq primer: T7; GTAATACGACTCACTATAGGCG.
 Location/Qualifiers

FEATURES

source

1..17

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/clone="024-017-B22"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatnucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Bet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAA 5408
17 AAAAAAAAAAAAAA 2

Db 17 AAAAAAAAAAAAAA 2

RESULT 790
B0591588/c 17 bp mRNA linear EST 06-DEC-2002
LOCUS DEFINITION E012616-024-017-Cl5-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION B0591588
VERSION B0591588
KEYWORDS B0591588.1 GI:26121171
SOURCE EST.
ORGANISM Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,W., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

TITLE
JOURNAL MEDLINE
PUBMED 2262189
12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishna@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: C column: 15
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
location/Qualifiers
1. 17
/organism="Beta vulgaris"
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/cultivar="KMS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188532"
/db_xref="taxon:161934"
/clone="024-017-Cl5"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"

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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatnucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Bet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5403 AAAAAAGAAAAATGA 5418
16 AAAAAAAAAAAAAATGA 1

Db 16 AAAAAAAAAAAAAATGA 1

RESULT 791
CF290854/c 17 bp mRNA linear EST 14-AUG-2003
LOCUS DEFINITION 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--01-A21, mRNA
sequence.
ACCESSION CF290854
VERSION CF290854.1 GI:33659887
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
location/Qualifiers
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source

Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5393 AAAAAATACAAAAA 5408
17 AAAAAAAAAAAAAA 2

Db 17 AAAAAAAAAAAAAA 2

RESULT 792
CF295807/c 17 bp mRNA linear EST 14-AUG-2003
LOCUS


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DEFINITION 30DGS--05-012.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa (japonica cultivar-group) cDNA clone 30DGS--05-012, mRNA
            sequence.
ACCESSION  CF295807
VERSION    CF295807.1 GI:33664840
KEYWORDS  EST.
SOURCE     Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiales; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 17)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
            source
            1..17
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultiyar="Nackdong"
            /db_xref="taxon:39947"
            /clone="30DGS--05-012"
            /tissue_type="leaf"
            /dev_stage="30 days after germination"
            /lab_host="E.coli DH10B"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAAATACAAAAA 5408
Db 16 AAAAAAAAAAAAAA 1

RESULT 793
CF298589/c 17 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION 7LEAF--02-A18.b1 Rice leaf plasmid cDNA clone 7LEAF--02-A18, mRNA
            sequence.
ACCESSION  CF298589
VERSION    CF298589.1 GI:33670350
KEYWORDS  EST.
SOURCE     Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiales; Oryzaceae; Oryza.
            1 (bases 1 to 17)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

JOURNAL
COMMENT

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FEATURES
            source
            Location/Qualifiers
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            /organism="Oryza sativa (japonica cultivar-group)"
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            /clone="7LEAF--02-A18"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5393 AAAAAAATACAAAAA 5408
Db 16 AAAAAAAAAAAAAA 1

RESULT 794
CF299639/c 17 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION 7LEAF--03-L20.b1 Rice leaf plasmid cDNA clone 7LEAF--03-L20, mRNA
            sequence.
ACCESSION  CF299639
VERSION    CF299639.1 GI:33671400
KEYWORDS  EST.
SOURCE     Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Euphorbiales; Oryzaceae; Oryza.
            1 (bases 1 to 17)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

JOURNAL
COMMENT

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RESULT 795
CF302447/c 17 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA
sequence.
ACCESSION CF302447 GI:33674208
VERSION CF302447.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 Eriartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
JOURNAL of Bioscience and Bioinformatics, Myongji University
COMMENT Yongsin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .17
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
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Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAA 5408
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 796
CF310219 17 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-M02, mRNA sequence.
ACCESSION CF310219 GI:33681980
VERSION CF310219.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 Eriartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
JOURNAL of Bioscience and Bioinformatics, Myongji University
COMMENT Yongsin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

```

Yongsin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

FEATURES
source
Query Match 0.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5393 AAAAAAAAAACAAAAA 5408
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 797
CF311499/c 17 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.
ACCESSION CF311499 GI:33683260
VERSION CF311499.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 Eriartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
JOURNAL of Bioscience and Bioinformatics, Myongji University
COMMENT Yongsin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match	0.2%	Score 12.8	DB 1	Length 17
Best Local Similarity	87.5%	Pred. No. 5.2e+02		
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OY	5400 TACAAAAAGAAAAA	5415		
DB	16 TAAAAA	1		
RESULT 798				
LOCUS	CF313013/c			
DEFINITION	ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-P19, mRNA sequence.			
ACCESSION	CF313013			
VERSION	CF313013.1	GI:33684774		
KEYWORDS	EST.			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.			
AUTHORS	1 (bases 1 to 17)			
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.			
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs			
COMMENT	Unpublished (2003)			
CONTACT	Contact: Nahm B.H.			
GENOMICS	Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University			
YONGJIN	Yongjin, Kyonggi, Korea			
TEL	Tel: 82 31 330 6193			
FAX	Fax: 82 31 321 6355			
EMAIL	Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.			
LOCATION	Location/Qualifiers			
FEATURES				
SOURCE	1..17			
ORGANISM	"Oryza sativa (japonica cultivar-group)"			
MOI	type="rRNA"			
CULTIVAR	"Nackdong"			
DB_XREF	"caxon:39947"			
CLONE	"ABF--08-P19"			
TISSUE	type="leaf"			
DEV_STAGE	"14 days after germination"			
LAB_HOST	"E.coli DH10B"			
CLONE_LIB	"ABF3-overexpressing transgenic rice plasmid CDNA library (ABF)"			
NOTE	"Vector: pCR4-TOPO; Site: 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."			
Query Match	0.2%	Score 12.8	DB 1	Length 17
Best Local Similarity	87.5%	Pred. No. 5.2e+02		
Matches 14	Conservative 0	Mismatches 2	Indels 0	Gaps 0
OY	5393 AAAAAATACAAAAA	5408		
DB	16 AAAAAA	1		
RESULT 799				
LOCUS	CF334566/c			
DEFINITION	JMT--03-O13.g1 AcJMT-overexpressing transgenic rice plasmid CDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-O13, mRNA sequence.			
ACCESSION	CF334566			
VERSION	CF334566.1	GI:33817460		
KEYWORDS	EST.			

SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
TITLE	Bukarete; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
JOURNAL	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
AUTHORS	Einhartoidesae; Oryzaceae; Oryza.
REFERENCE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myungji University Yongsin, Kyeonggi, Korea Tel.: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahmbio.myonngji.ac.kr.
COMMENT	location/Qualifiers
FEATURES	1..17
SOURCE	/organism="Oryza sativa (japonica cultivar-group)" /mol_type="mrna" /cultivar="Nackdong" /db_xref="taxon:39947" /clone="JMT-03-013" /tissue_type="leaf" /dev_stage="14 days after germination" /lab_host="E.coli DH10B" /clone_lib="AclJMUT-overexpressing transgenic rice plasmid CDNA library (JMT) " /note="Vector: PCR4-TOP0; Site 1: EcoRI; oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."
Query Match	0.2%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5% ; Pred.No.5.2e+02; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Dy	5393 AAAAAAAAAACAAAAAA 5408 Db 17 AAAAAAAAAAAAAAAAAA 2
RESULT 800	
CF301057/C	18 bp mRNA linear EST 15-AUG-2003
LOCUS	7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION	sativa [japonica cultivar-group] CDNA clone 7LEAF--05-M05, mRNA sequence.
ACCSSION	CF301057 GI:33672818
VERSION	EST.
KEYWORDS	Oryza sativa (japonica cultivar-group)
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Einhartoideae; Oryzeae; Oryza.
REFERENCE	1 (bases 1 to 18) Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongjin, Kyeonggi, Korea Tel.: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahmbio.myonngji.ac.kr.
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SOURCE	/organism="Oryza sativa (japonica cultivar-group)" /mol_type="mrna"

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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--05-M05"
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/dev_host="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5393 AAAAAAATACAAAAA 5408
        ||||| |||||
        17 AAAAAAAAAAAAAAAAAA 2

RESULT 801
LOCUS      CF329285
DEFINITION  CF329285 18 bp mRNA linear EST 18-AUG-2003
             NAEL--04-122.b1 Rice callus plasmid cDNA library (NAEL) Oryza
             sativa (japonica cultivar-group) cDNA clone NAEL--04-122, mRNA
             sequence.
ACCESSION   CF329285
VERSION     CF329285.1 GI:33806806
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 18)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, Greengene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
            Location/Qualifiers
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FEATURES
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DEFINITION  2M0010G08F Mouse 10kb plasmid UNGCM library Mus musculus genomic
            clone UNGC2M0010G08 F, genomic survey sequence.
ACCESSION   A2776487
VERSION     A2776487.1 GI:12904111
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
            Mus musculus
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 27)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Nedderhousen,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
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            Class: plasmid ends
            High quality sequence stop: 27.
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                /clone_lib="Mouse 10kb plasmid UNGCM library"
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                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pMD42 (g1473214[gB]AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

Query Match      0.2%; Score 12.8; DB 1; Length 27;
Best Local Similarity 70.8%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      224 TCTCCCTCACCTTCACCTTCCT 247
        ||||| ||||| |||||
        Db      26 TCTACTCTCTCTCTCTCTCTCT 3

RESULT 803
LOCUS      AJ662980
DEFINITION  AJ662980 21 bp mRNA linear EST 28-JUN-2004
            CSORAN09 Sus scrofa cDNA clone C0000024_P01, mRNA

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sequence.
ACCESSION AJ662980
VERSION AJ662980.1 GI:49347103
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
JOURNAL embryo development in pigs and cattle
COMMENT Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pbuescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES
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NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
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Best Local Similarity 78.9%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 569 TGAAGAAGAGAGAGCTGAA 587
Db 3 TGAAGAAGTGGGATGCA 21
RESULT 804
ACCESSION AJ242914
LOCUS AJ242914
DEFINITION 26 bp DNA linear GSS 29-SEP-2000
clone UUCG1M0076C22 F, genomic survey sequence.
ACCESSION AJ242914
VERSION AJ242914.1 GI:10420628
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

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Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 22
Seq primer: CGTTGTAAGACGAGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
FEATURES
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/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passages through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD4 (g14732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.2%; Score 12.6; DB 1; Length 26;
Best Local Similarity 78.9%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 969 AGAATCTCTCTCTCTCTC 987
Db 1 AGAATCTCTCTCTCTCTC 19
RESULT 805
ACCESSION AZ873739
LOCUS AZ873739
DEFINITION 27 bp DNA linear GSS 21-FEB-2001
clone UUCG2M0187C08 R, genomic survey sequence.
ACCESSION AZ873739
VERSION AZ873739.1 GI:13082111
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

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Plate: 0187 row: C column: 08
Seq primer: CACACAGAAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES

source

1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U9C2M0187C08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U9C1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 12.6; DB 1; Length 27;
Best Local Similarity 66.7%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 975 CTCTGCTCACTCTCTACCAAGCTT 1001
Db 1 CTCTCTCTCTCTCTCTCAAGCTT 27

RESULT 806

CF301021

LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-L10-91 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-L10, mRNA sequence.

ACCESSION CF301021 GI:33672782

VERSION CF301021.1

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

JOURNAL Contact: Nahm B.H.
Genetics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. 14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--05-L10"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5394 AAAAAATCAAAA 5407
Db 1 AAAAAATCAAAA 14

RESULT 807

CF327203/c

LOCUS 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-J16, mRNA sequence.

ACCESSION CF327203 GI:33802665

VERSION

CF327203.1

KEYWORDS

EST.

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

CONTACT: Nahm B.H.
Genetics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source Location/Qualifiers
1. 14
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-J16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5402 CAAAAAGAAAAA 5415
Db 14 CAAAAAGAAAAA 1

RESULT 808

LOCUS CF290849 15 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-A17, mRNA sequence.

ACCESSION CF290849

VERSION CF290849.1 GI:33659882

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriatropidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-A17"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5395 AAAAAATCAAAAA 5408
|||||
1 AAAAAATCAAAAA 14

RESULT 809

LOCUS CF296652

DEFINITION 30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--07-C02, mRNA sequence.

ACCESSION CF296652

VERSION CF296652.1 GI:33665685

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriatropidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--07-C02"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5402 CAAAAAGAAAAA 5415
|||||
15 CAAAAAGAAAAA 2

RESULT 810

LOCUS A695224

DEFINITION A695224 Bos taurus cDNA clone KN261-046_F05, mRNA sequence.

ACCESSION A695224

VERSION A695224.1 GI:49428643

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 16)

AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.

TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

JOURNAL Unpublished (2004)

COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector: pBluescriptII (SK+) R. Site1: EcoRI R. Site2: SmaI 5' Seq Primer T3 Normalised library constructed from bovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.atkgenomics.org.

FEATURES

source

1..16
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-046_F05"
/tissue_type="ovary"
/clone_lib="KN261"
/note="Vector: pBluescriptII (SK+); Site 1: EcoRI; Site 2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."

Query Match 0.2%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 38 CCAGCAGCCCGGG 51
|||||
14 CCGCAGCCCGGG 1


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RESULT 811
BOS90207/c      16 bp  mRNA  linear  EST 06-DEC-2002
LOCUS
DEFINITION
BOS90207
ACCESSION
BOS90207
VERSION
BOS90207.1 GI:26119790
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
plant J. 32 (5), 845-857 (2002)
22362189
JOURNAL
MEDLINE
PUBMED
12472698
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 16 Std Error: 0.00
Plate: 19 row: 0 column: 15
Seq primer: T7: GTATACGACTCCTACTATAGAGCC.
FEATURES
source
1. 16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189913"
/db_xref="taxon:161934"
/clone="024-019-015"
/tissue_type="storage root"
/lab_host="EMD10B"
/clone_1lb="MPiZ-ADIS-024-storage root"
/note="Vector: PCMVSPORT6, Site_1: SalI, Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinanzelebener Saat-zucht AG Bindeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 0.24; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5402 CAAAAAGAAAAA 5415
Db 16 CAAAAAGAAAAA 3

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthroideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaah@gbdo.com, bhnaah@bio.myongji.ac.kr.
FEATURES
source
1. 16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-09-D06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_1lb="OSHAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI, Callus was
created with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

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RESULT 813
CF327923/c      16 bp  mRNA  linear  EST 18-AUG-2003
LOCUS
DEFINITION
CF327923
ACCESSION
CF327923
VERSION
CF327923.1 GI:33804096
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthroideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaah@gbdo.com, bhnaah@bio.myongji.ac.kr.
FEATURES
source
1. 16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-J18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_idb="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5402 CAAAAGAGAAAAA 5415
Db 16 CAAAAGAGAAAAA 3

RESULT 814
CF328223/c
LOCUS
DEFINITION
CF328223 16 bp mRNA linear EST 18-AUG-2003
NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--03-A10, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CF328223.1 GI:33804692
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
JOURNAL
COMMENT
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..16
location="Oryza sativa (japonica cultivar-group)"
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-A10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_idb="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5402 CAAAAGAGAAAAA 5415
Db 16 CAAAAGAGAAAAA 3

RESULT 815
AM250784/c
LOCUS
AM250784 17 bp mRNA linear EST 07-JAN-2000

DEFINITION
2822335.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822335 3',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AM250784.1 GI:6593777
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
JOURNAL
COMMENT
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2822335.5prime
Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov,
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (ILNLD) DNA Sequencing by: Berkeley MGC sequencing
project clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/ILNLD at:
www.bio.lit.edu/birop/image/image.html Baee Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila genome project. University of Washington Genome Center:
<http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very low
quality sequence: trace file contained 17 contiguous distinct peaks
following vector sequence.
Plate: L1CM9 row: C column: 8.
Location/Qualifiers

FEATURES
source
1..17
location="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822335"
/tissue_type="mammary cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_idb="NIH_MGC_7"
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 12.4; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 5.8e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5403 AAAAAAGAAAAATGAA 5419
Db 17 AAAAAAGAAAAATGAA 1

RESULT 816
CF297251/c
LOCUS
DEFINITION
CF297251 17 bp mRNA linear EST 14-AUG-2003
30DGS--07-P12.g1 Rice leaf plasmid cDNA library 1 (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--07-P12, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CF297251.1 GI:33666284
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

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 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5402 CAAAAGAGAAAAA 5415
 Db 16 CAAAAGAGAAAAA 3

RESULT 817 17 bp mRNA linear EST 15-AUG-2003
 CF298341/c 7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-K24, mRNA
 sequence.

ACCESSION CF298341 GI:33670102
 VERSION CF298341
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
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 1..17
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 Db 16 CAAAAGAGAAAAA 3

Search completed: November 2, 2004, 10:37:00
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